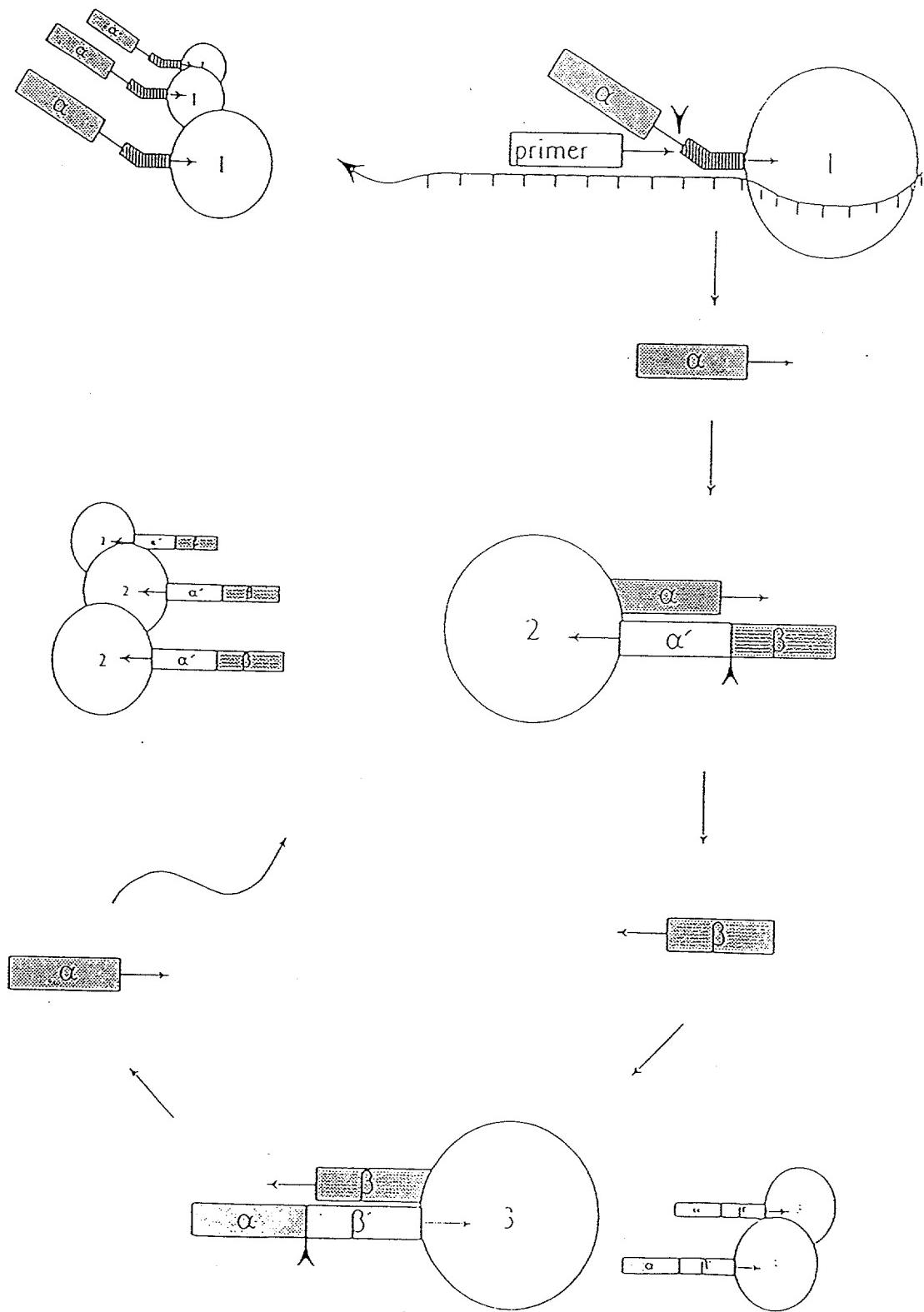


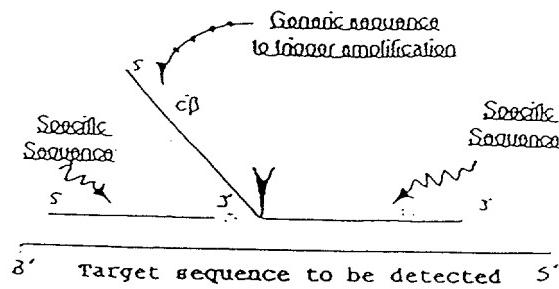
FIGURE 1A



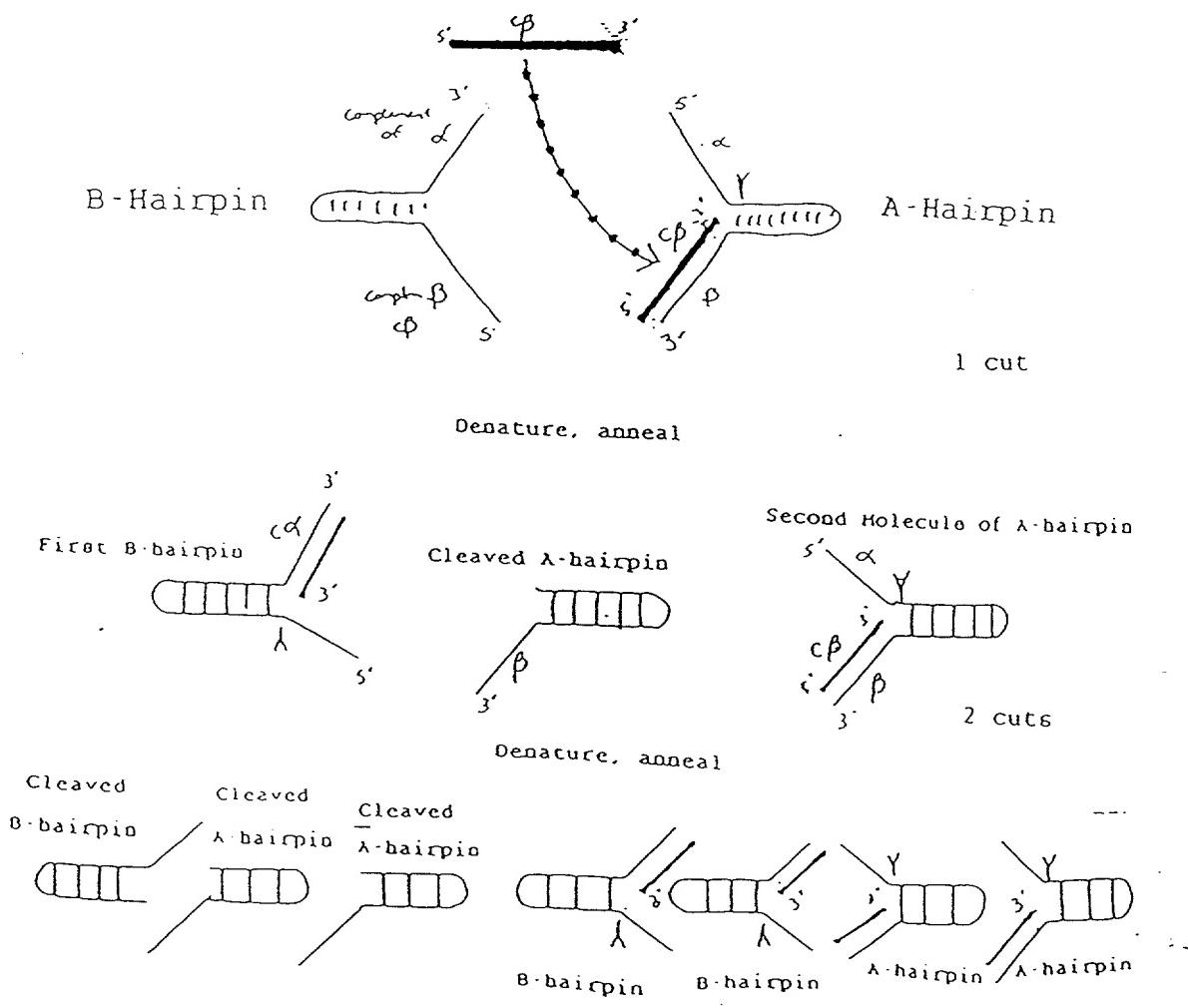
1/127

FIGURE 1B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION



卷之三

FIGURE 2

3/127

On April 10, 1945, the *U.S. News and World Report* published an article by James M. Flanagan, entitled "The War in Europe," which contained the following statement:

FIGURE 2 (cont'd)

4/127

FIGURE 2 (cont'd)

5/127

PSEUDO-SEQUENCE

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	CCCCGXCCTCCCAAGGACCTGGCCCTTACGGCACCCCCXGACCTCTGCCCTACCGC	
OKAPTAO	(SEQ ID NO:1)	A.....AG.....C.....A.....AG.....C.....A.....T.....C.....C.....	118c
QWAPTR	(SEQ ID NO:2)	AA.....G.....G.....G.....G.....G.....G.....T.....A.....A.....	118l
QWAPTH	(SEQ ID NO:3)	C.....C.....C.....C.....C.....C.....C.....G.....A.....G.....	112c
MAJORITY		ACCCATGCCCTCCCTAACACCACCCCCCTGCCCTACCGC	
OKAPTAO	T.....T.....T.....T.....T.....T.....T.....	118c
QWAPTR	T.....T.....T.....T.....T.....T.....T.....	118l
QWAPTH	T.....T.....T.....T.....T.....T.....T.....	119c
MAJORITY		CCCCGACTGGACGGAGAXGGGGGAGCCCCCTCCCTACCGC	
OKAPTAO		C.....G.....G.....G.....T.....A.....G.....C.....C.....	125
QWAPTR	A.....A.....A.....A.....G.....C.....C.....	125
QWAPTH	C.....CCC.....C.....C.....C.....C.....	126
MAJORITY		CCCCCTGAGGACACCCCTCCCTTACCAACCCCTTCCCCCCTT	
OKAPTAO		A.....G.....A.....A.....AC.....C.....G.....G.....	132
QWAPTR	A.....A.....AC.....C.....G.....G.....C.....	132
QWAPTH	C.....A.....C.....C.....C.....C.....A.....	133
MAJORITY		CCCCACATGCCAACCCCCCTGCCCTGGACCTTCCCCCTACCGC	
OKAPTAO		G.....C.....C.....G.....C.....C.....T.....A.....	135
QWAPTR	C.....C.....C.....C.....C.....A.....C.....	139
QWAPTH	T.....T.....T.....T.....T.....C.....C.....	140

FIGURE 2 (cont'd)

FIGURE 2 (cont'd)

8/127

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	ACCTTCCAAAGCTCCGCCCCATTAGAACCCCTGGACCAAGCCAGGCTACCCCGA	2161
QHAFTH (SEQ ID NO:1)	2161
QHAFTR (SEQ ID NO:2)	A.....	2161
QHAFTH (SEQ ID NO:3)	A.....	2161
MAJORITY	CCCTCTTCCGGCCCCCTTACGGTCCCCGACCTCAACGGCCCCGACCCGCCCCGGCA	2171
QHAFTH	C.....	2234
QHAFTR	A.....	2231
QHAFTH	A.....	2240
MAJORITY	CGCCATGGCCCTTCAACATGCCATGCCACCCGACCCGACCCGACCCGACCCGAC	2304
QHAFTH	2301
QHAFTR	2310
MAJORITY	TTCGGCCGCTTCAAGAAATGGGGCCACGGATGCCCTCCIXCAGCTCCACCCACCC	2371
QHAFTH	A.....	2380
QHAFTR	2380
QHAFTH	2444
MAJORITY	CCAAAGACCCCCCACGCGGCTTCCGAAACGACCCGACCCGACCCGACCCGACCC	2441
QHAFTH	A.....	2450
QHAFTR	2450

9/127

FIGURE 2 (cont'd)

FIGURE 3

MAJORITY (SEQ ID NO:8) HXAKHLPLFEPKGAVLILVQCHHLAYRITFALKGLITSGEPUQAVYCFAKSLLKALKEDCDAVXUVFOAK		
IAD PRO (SEQ ID NO:4)	R C	H
TR PRO (SEQ ID NO:5)	V . V . . .
TM PRO (SEQ ID NO:6)	E	Y K . F . .
7c		
MAJORITY		
APSF RHEAYEAYKAGRAPTPEDPROLALIKELVOLLCLXRLLEVPGYEADOVLAIIAKKAEKXCYEVRII		
IAD PRO	A	S
TR PRO	V	R
TM PRO	F T	
14		
MAJORITY		
IAQROLYOLLSORIAVLHPEGYLTPAHLWEKYGLAPEOWVOYRALXGOPSOKLPGVKCIGEXTAXKLLX		
IAD PRO	K	R
TR PRO	E	A
TM PRO	Y	I
2		
MAJORITY		
EYCSLEHLLKHLORVUKP. XXRAEKIXAHMEOLXLSXXLSSXVRIOLPLEUDAXRREPDORSECLRRAFLS		
IAD PRO	A	K
TR PRO	O	R
TM PRO	SL	CR
2		
MAJORITY		
CSLLHEFCGLEXPKALEEAPHYPPPEGAFAVUCFVLSRPEPKHXAOPUXGLROLKEV		
IAD PRO	S	C
TR PRO	G	R
TM PRO	A	A
3		

FIGURE 3 (cont'd)

	Majority (SEQ ID NO:8) RCLIAKOLAVLALREFCQLXPGDOPMILAYLLLOPSHTTPEGUARRYGCETWICACERALLSERLFXH		
TAO PRO	(SEQ ID NO:4)	S.....S.....G.....C.....P.....	488
TR PRO	(SEQ ID NO:5)	I.....F.....E.....	487
TH PRO	(SEQ ID NO:6)	S.....V.....A.....H.....	490
Majority			
TAO PRO	R.....R.....R.....	A.....A.....A.....	
TR PRO	K.....E.....K.....	E.....V.....L.....	
TH PRO	H.....H.....H.....		
Majority			
TAO PRO	R.....R.....R.....	A.....A.....A.....	SSC
TR PRO	K.....E.....K.....	E.....V.....L.....	SS7
TH PRO	H.....H.....H.....	V.....S.....S.....	SSC
Majority			
TAO PRO	R.....R.....R.....	O.....I.....O.....	621
TR PRO	K.....E.....K.....	V.....V.....A.....	621
TH PRO	H.....H.....H.....	A.....A.....A.....	63
Majority			
TAO PRO	R.....R.....R.....	O.....O.....O.....	69
TR PRO	S.....S.....S.....	G.....S.....G.....	69
TH PRO	X.....X.....X.....	V.....V.....V.....	70

000000000000000000000000

FIGURE 3 (cont'd)

MATERIAL (SEQ ID NO:8) S S P K V R A K I E K I L E F C R A R C Y U E T I I G C R A R C Y U P O L H A R V U K S U R E @ A E R H M F W U O C I @ A O U M X L A M V K I
IAQ PRO (SEQ ID NO:4)
R PRO (SEQ ID NO:5)
M PRO (SEQ ID NO:6)

MAJORITY
F P A L X E H C A R M L L Q V H O E L V L E A P K X R A E X V A A L A K E V R E G V Y P L A V P L E V E V G X G E D W L S A X E X
I A Q PRO
R PRO
M PRO

83
83
83
83

FIGURE 4

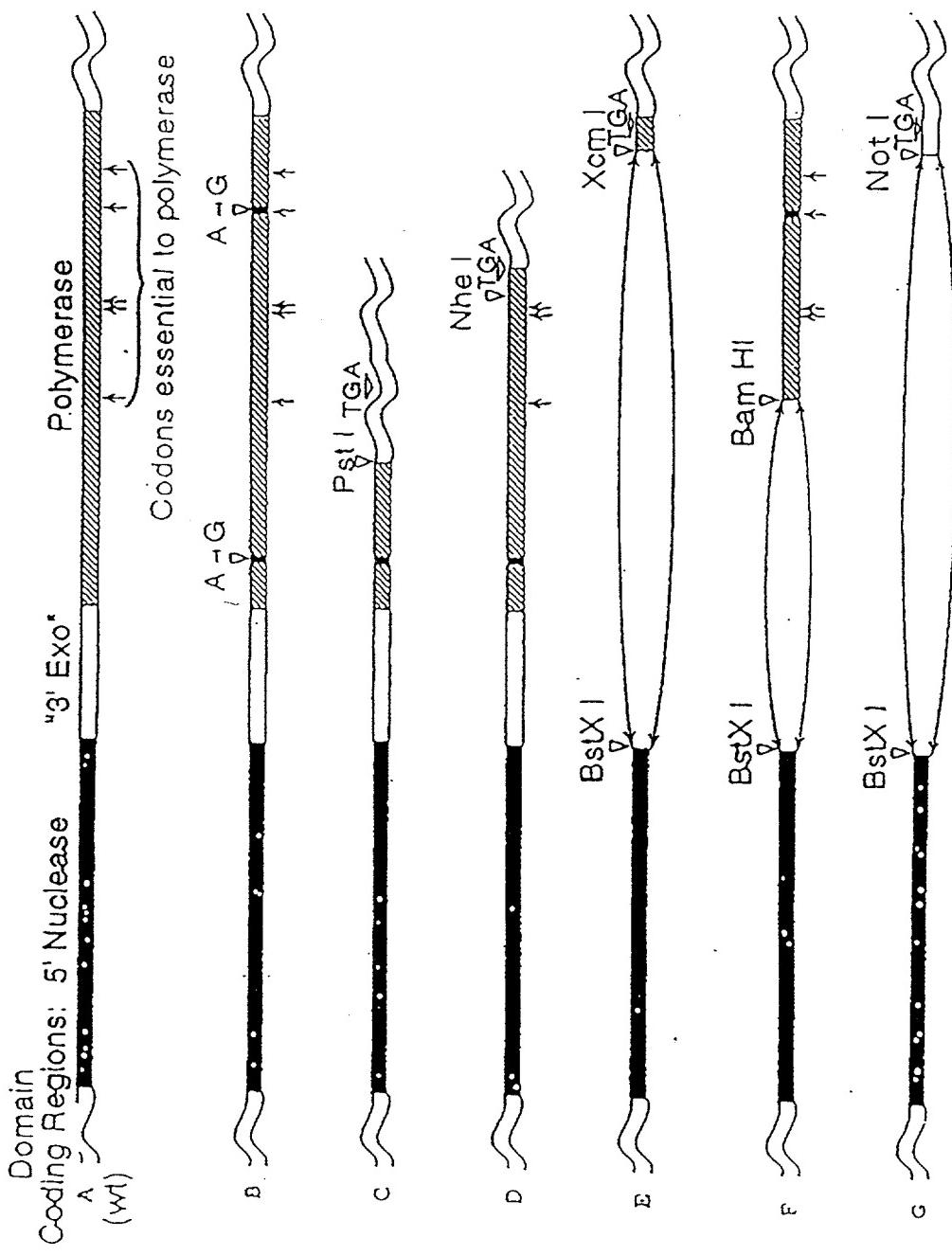


FIGURE 5

Genes for Wild-Type and Pol(-) DNAPL

Domain Coding Regions: 5' Nuclease
A ~ (wt)

15/127

Polymerase

Exo^x

Polymerase

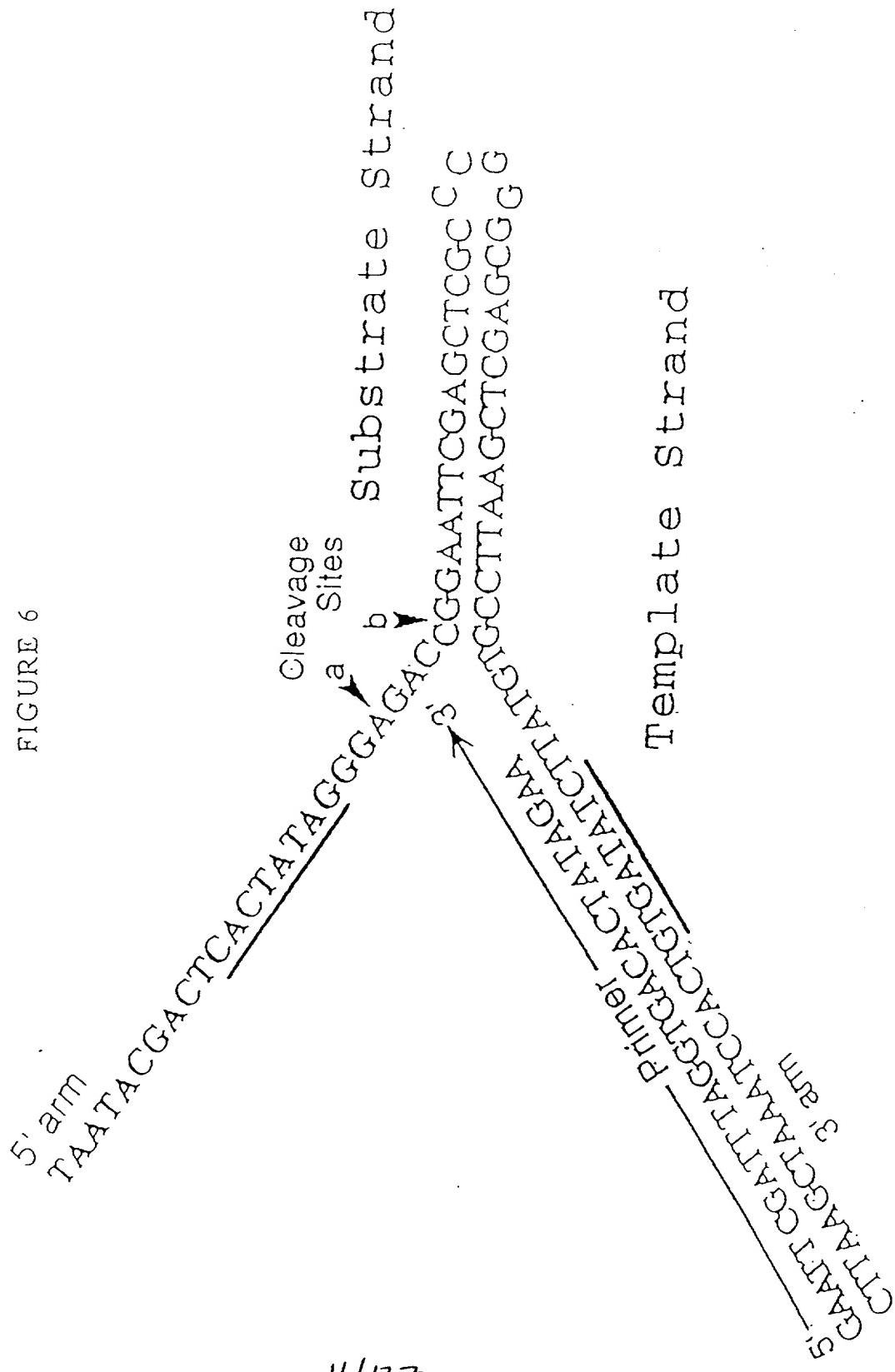
is essential to polymerase

Codons essential to polymerase

上

Diagram B shows a vertical line with a hatched section at the top and a white section below it. The bottom part of the line is solid black with small white dots. At the very bottom, there are two wavy lines pointing outwards from the sides.

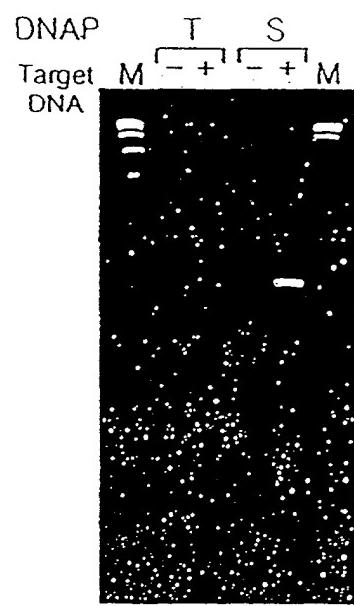
FIGURE 6



16/127

09684335 400500

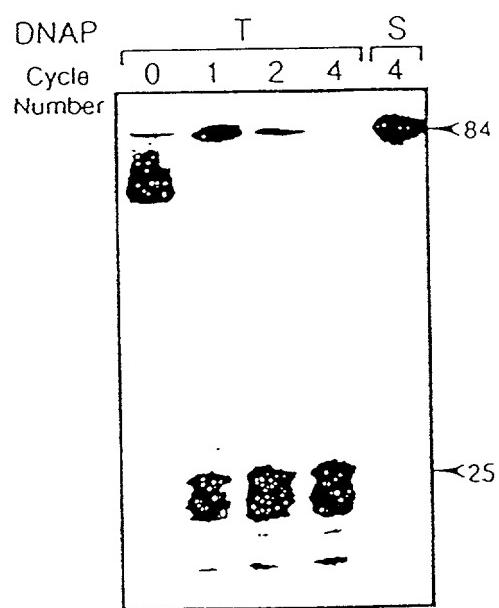
FIGURE 7



17/127

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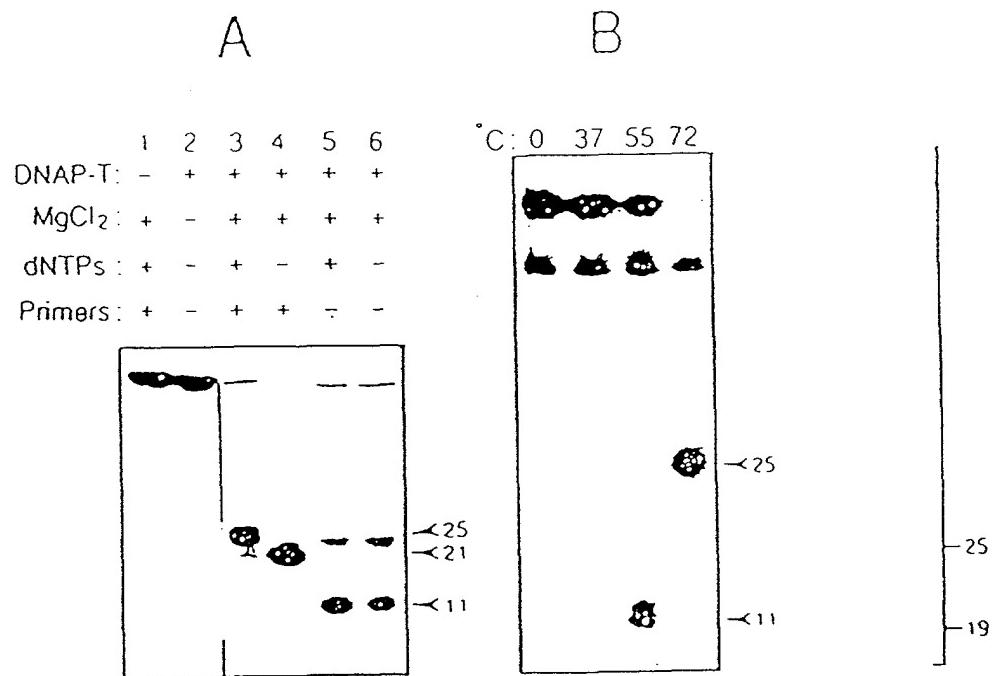
FIGURE 8



18/127

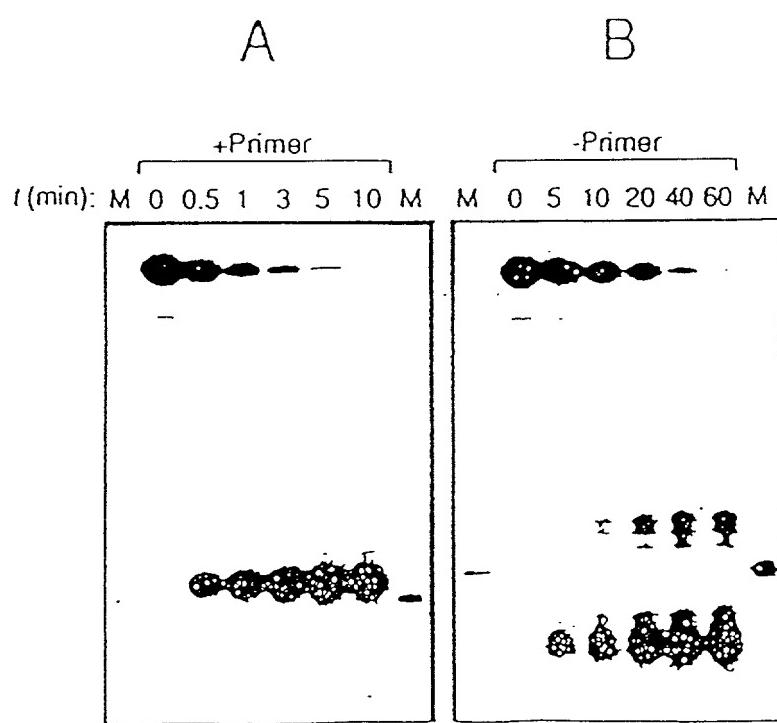
09634305 4366500

FIGURE 9



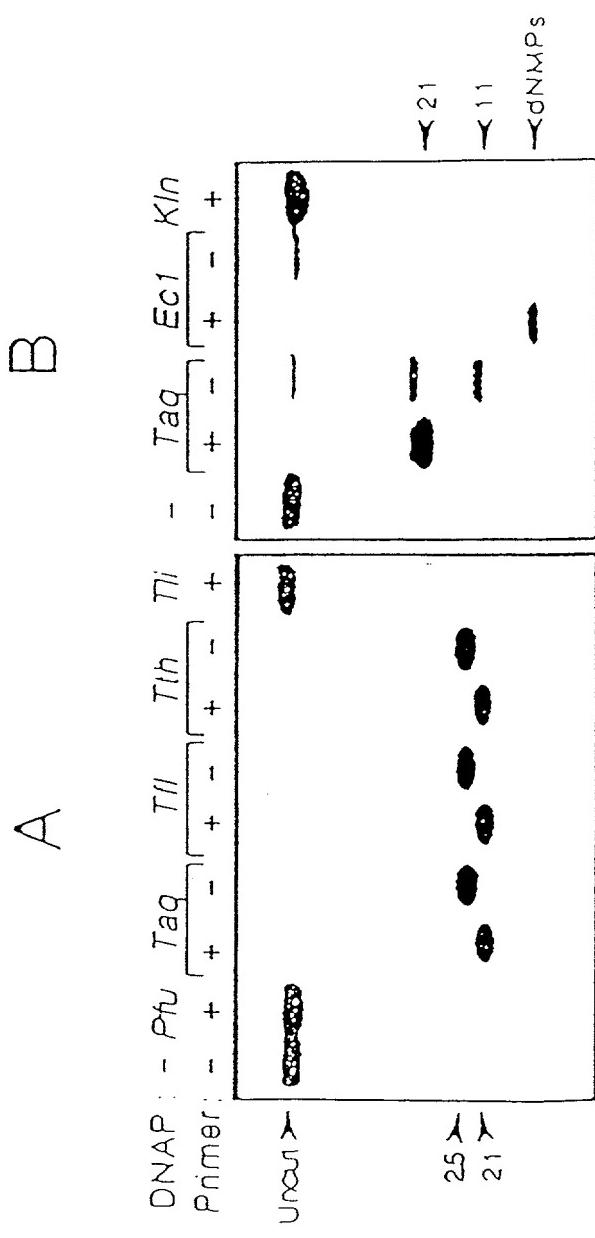
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FIGURE 10



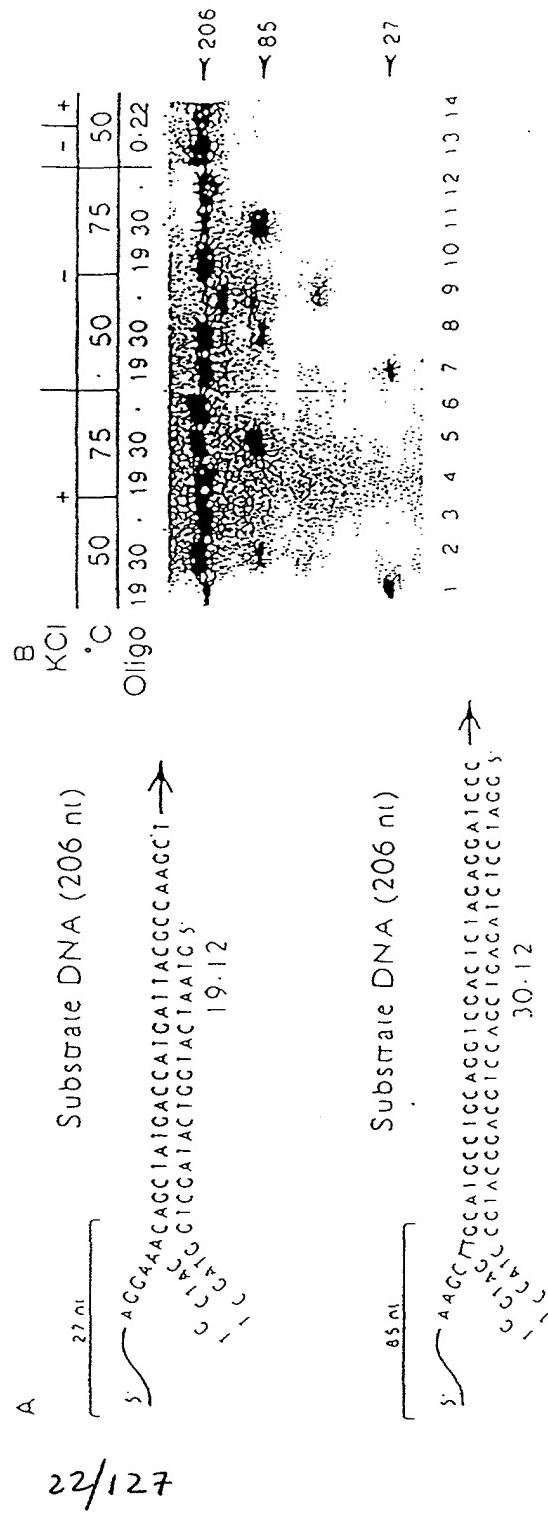
DNA Sequencing

FIGURE 11



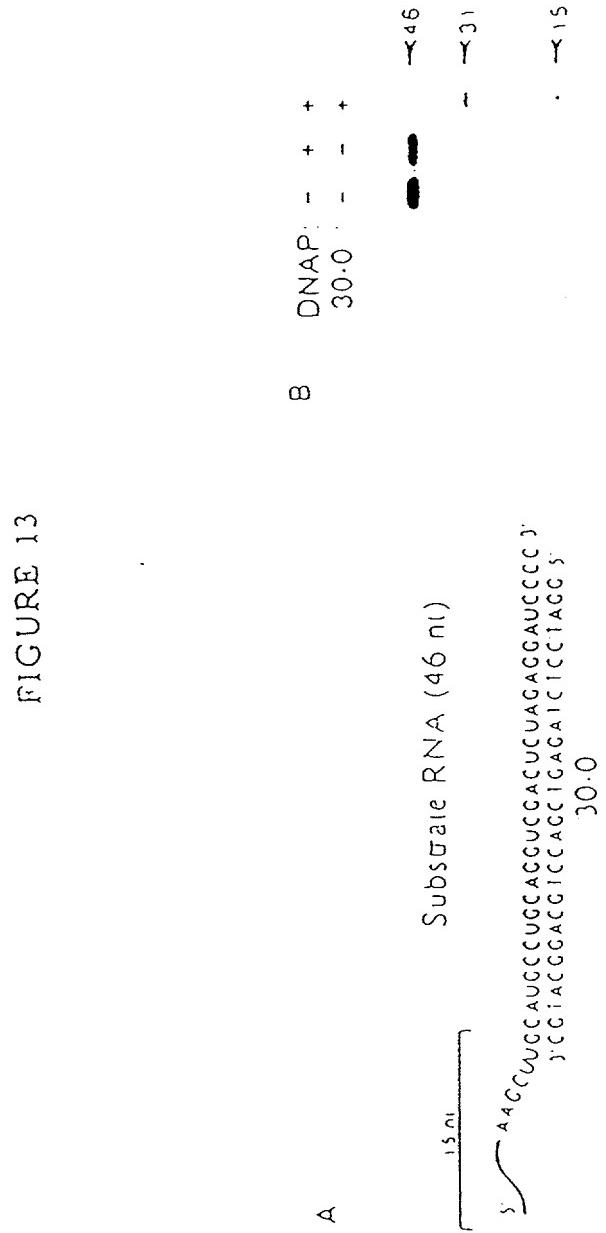
THE JOURNAL OF CLIMATE

FIGURE 12



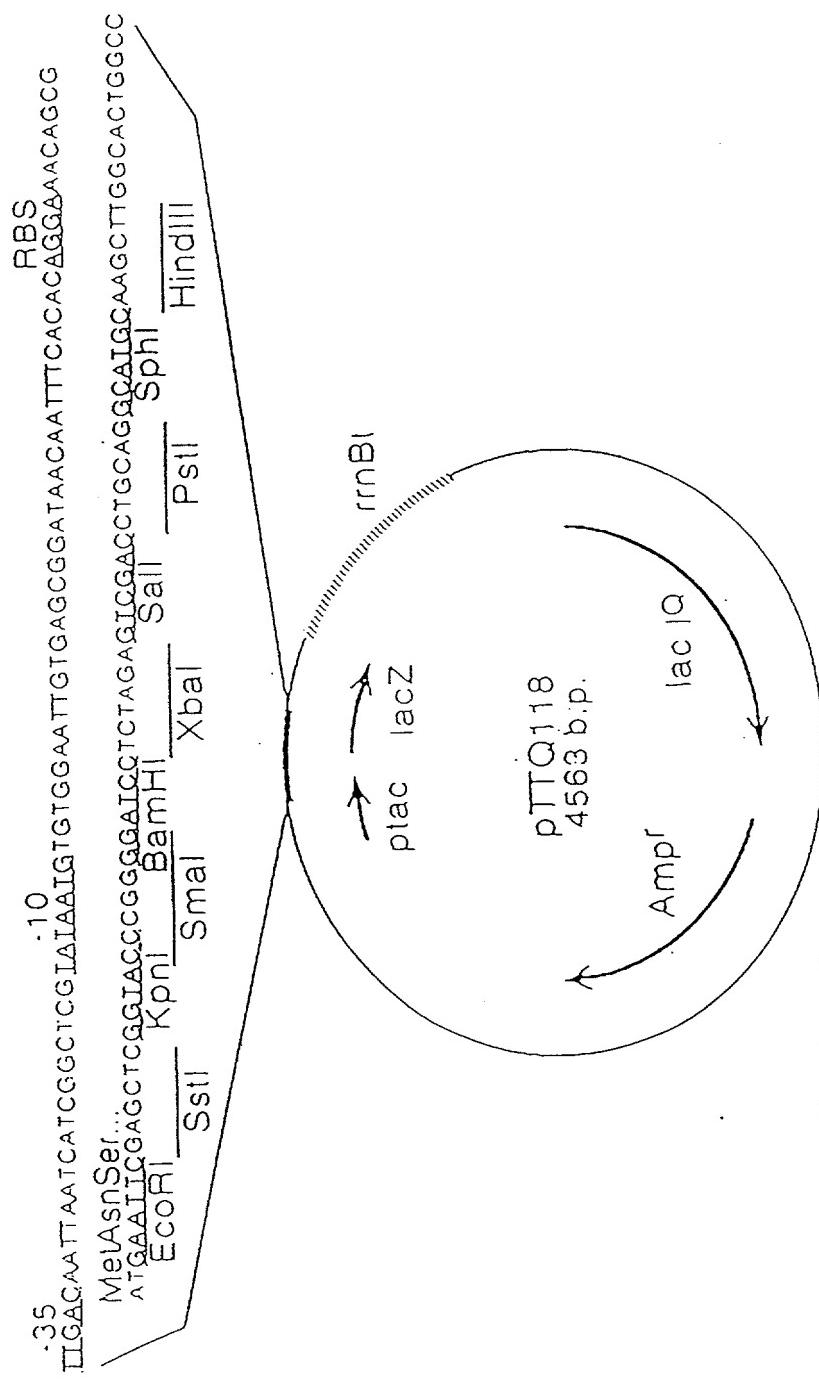
23/127

FIGURE 13



23/127

FIGURE 14



RBS: Ribosome binding site

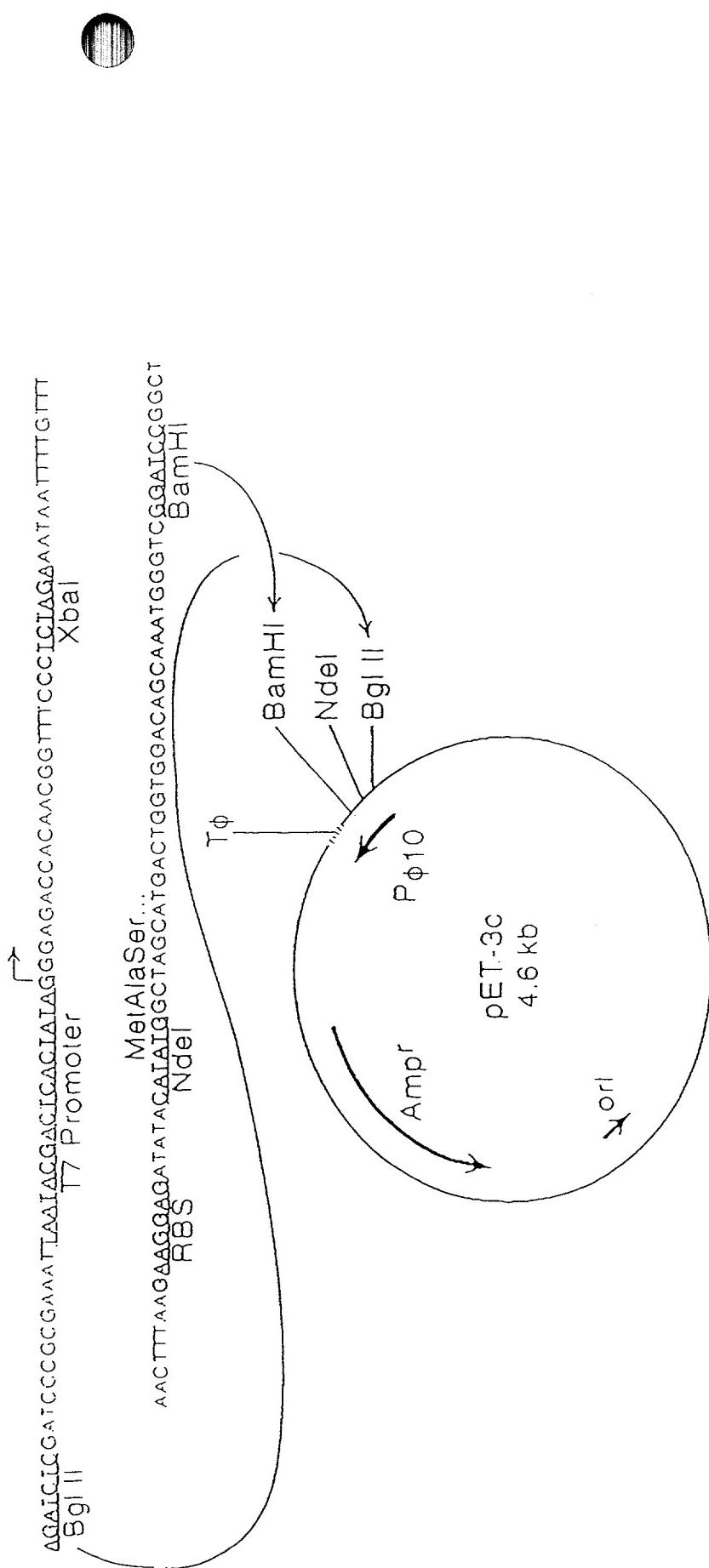
plac: Synthetic lac promoter

lac I^Q: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment

rrnB1: *E. coli* rrnB transcription terminator

FIGURE 15



25/127

$P_{\phi 10}$: Bacteriophage T7 $\phi 10$ promoter

$T\phi$: T7 ϕ Terminator

RBS: Ribosome binding site

FIGURE 16

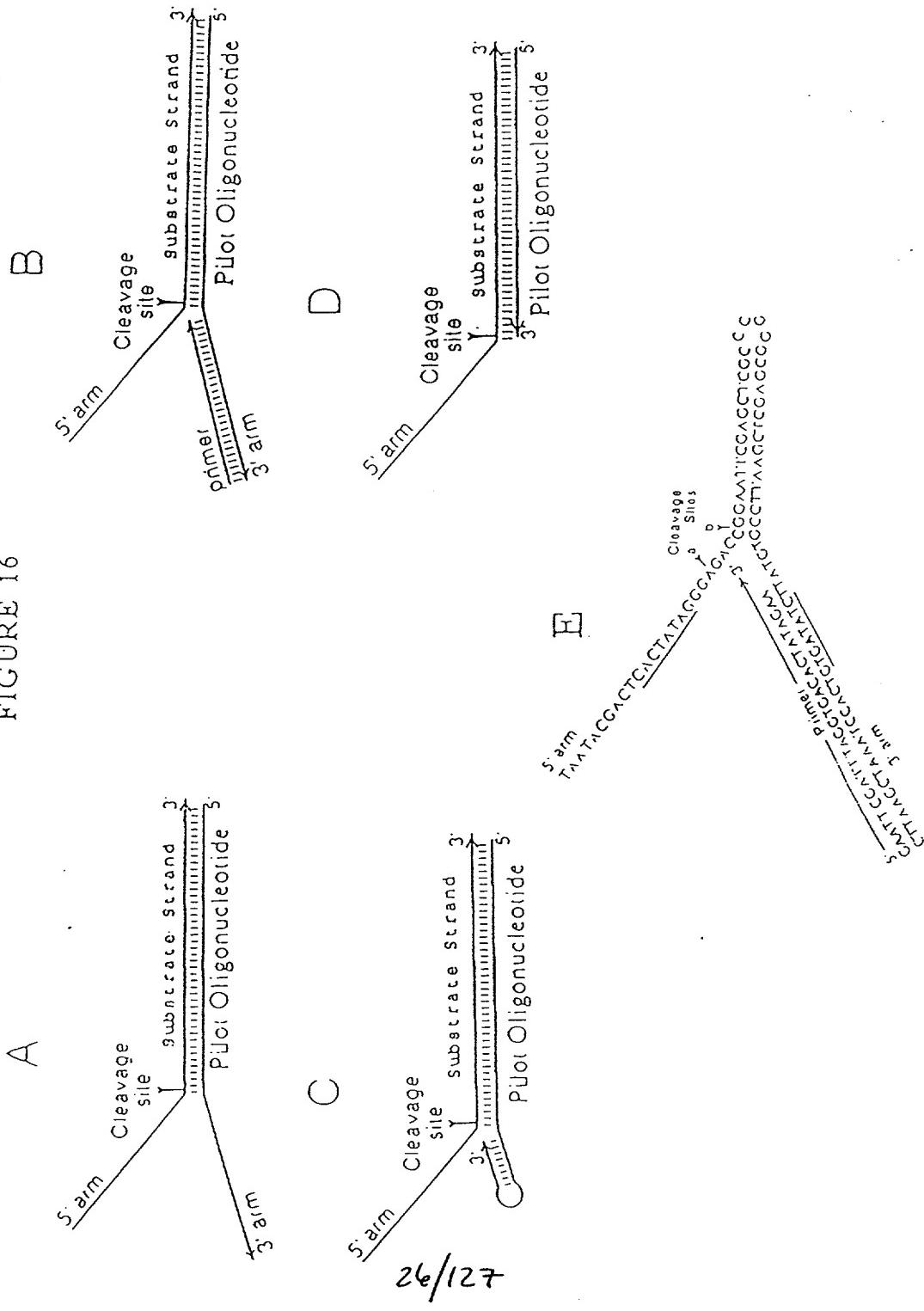


FIGURE 17

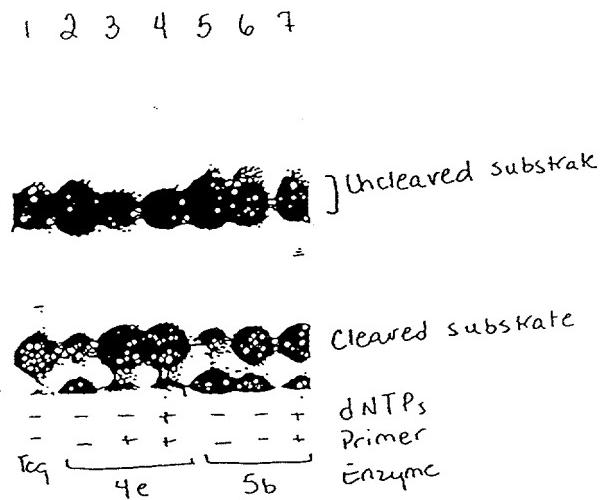
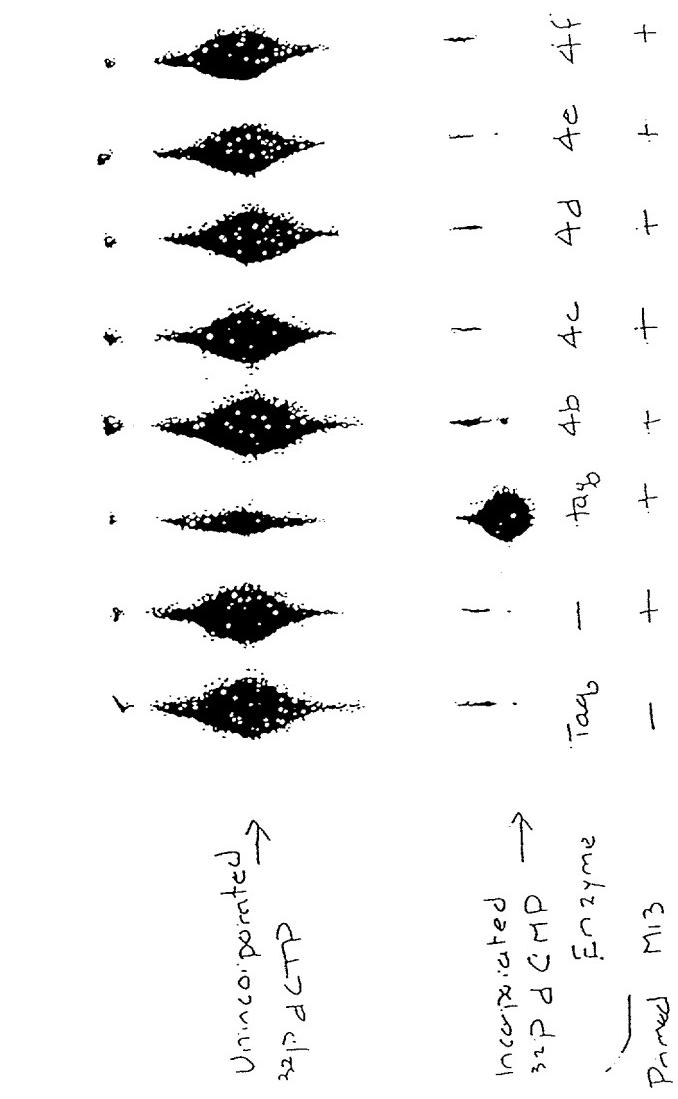


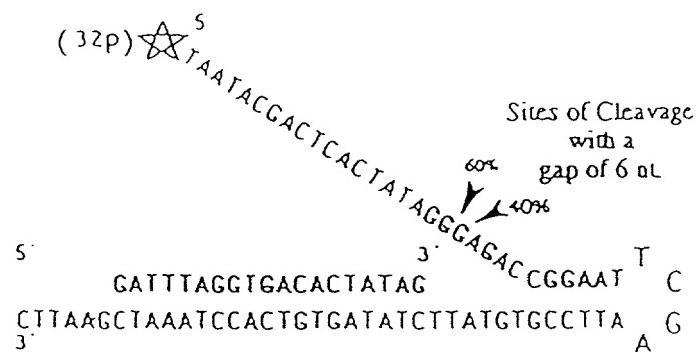
FIGURE 18



28/127

FIGURE 19

A



B

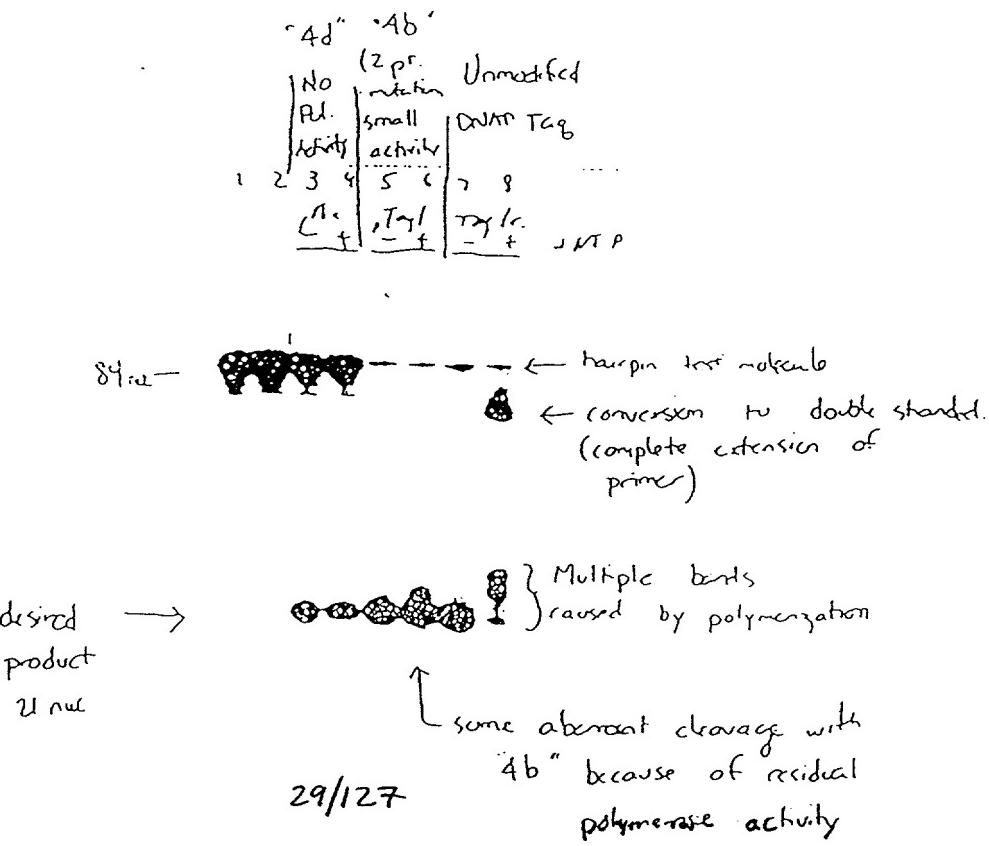
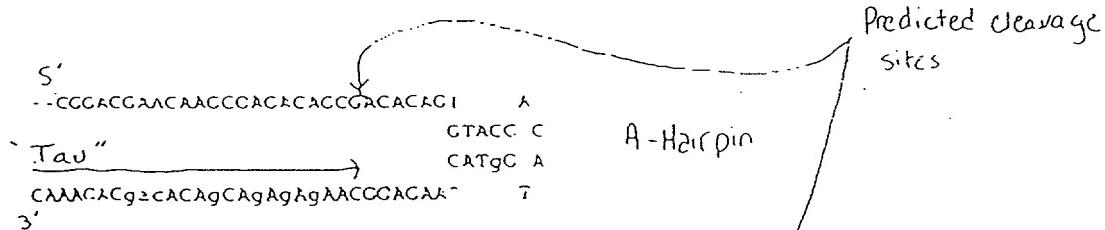
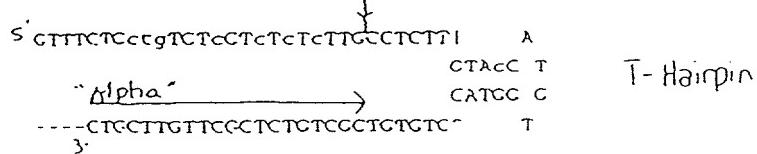


FIGURE 20

A



Sixty

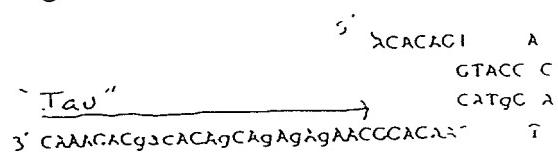


B

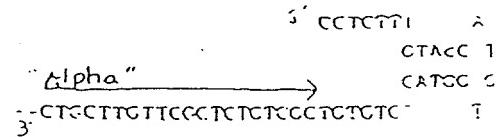
Sequence of alpha primer

5' GAC CAA CAC CCC AGA CAG CC 3'

C



Cleaved A-Hairpin



Cleaved T-Hairpin

D

$$T_{\text{top}} = T \cdot \text{Exp}(\rho_{\text{in}})$$

Bottom: A. Hair

१०८

F-22

۱۸۰

Nla III

HgiC i

Nla IV
S. 1

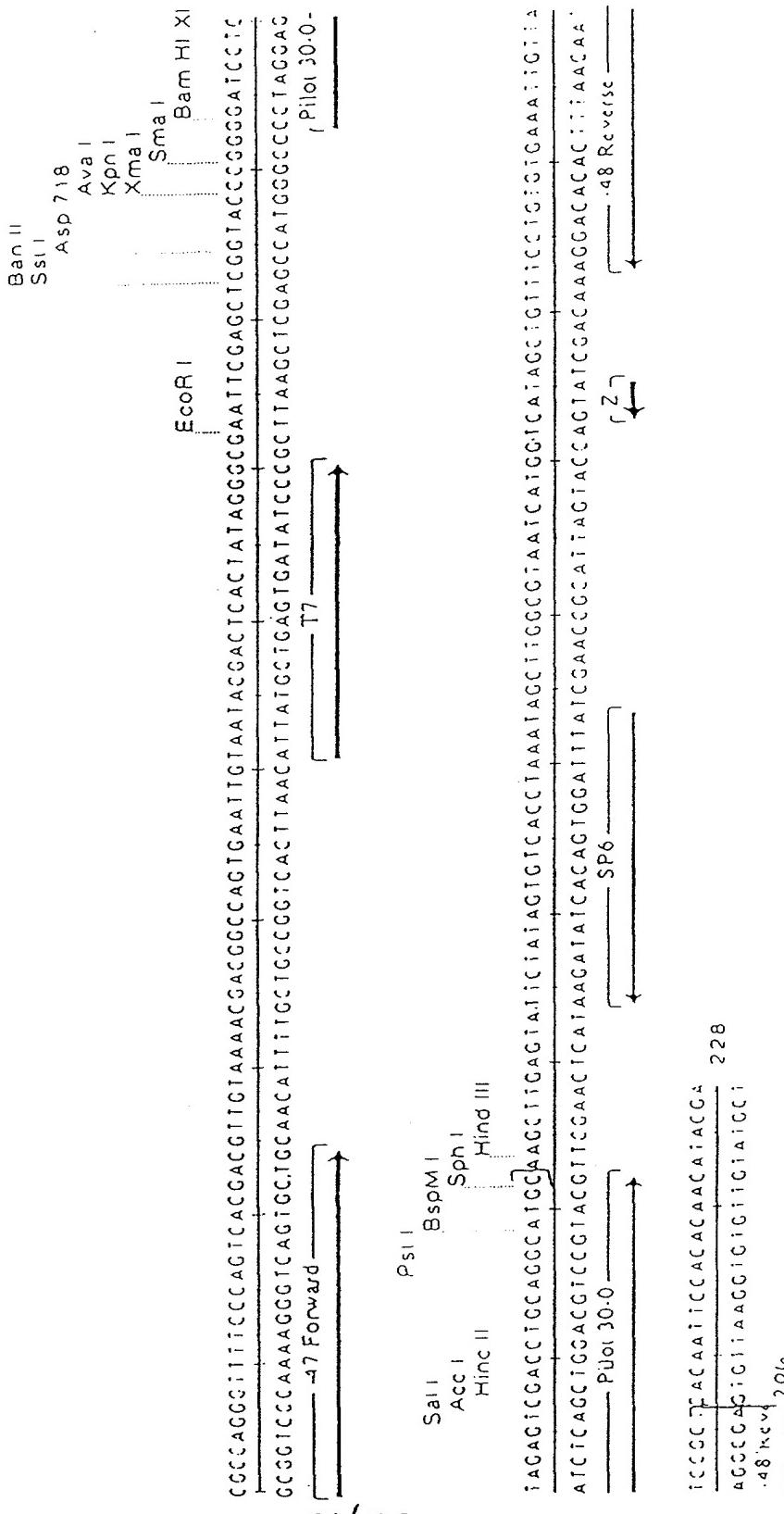
Hsa 1

B3mAl

30/127

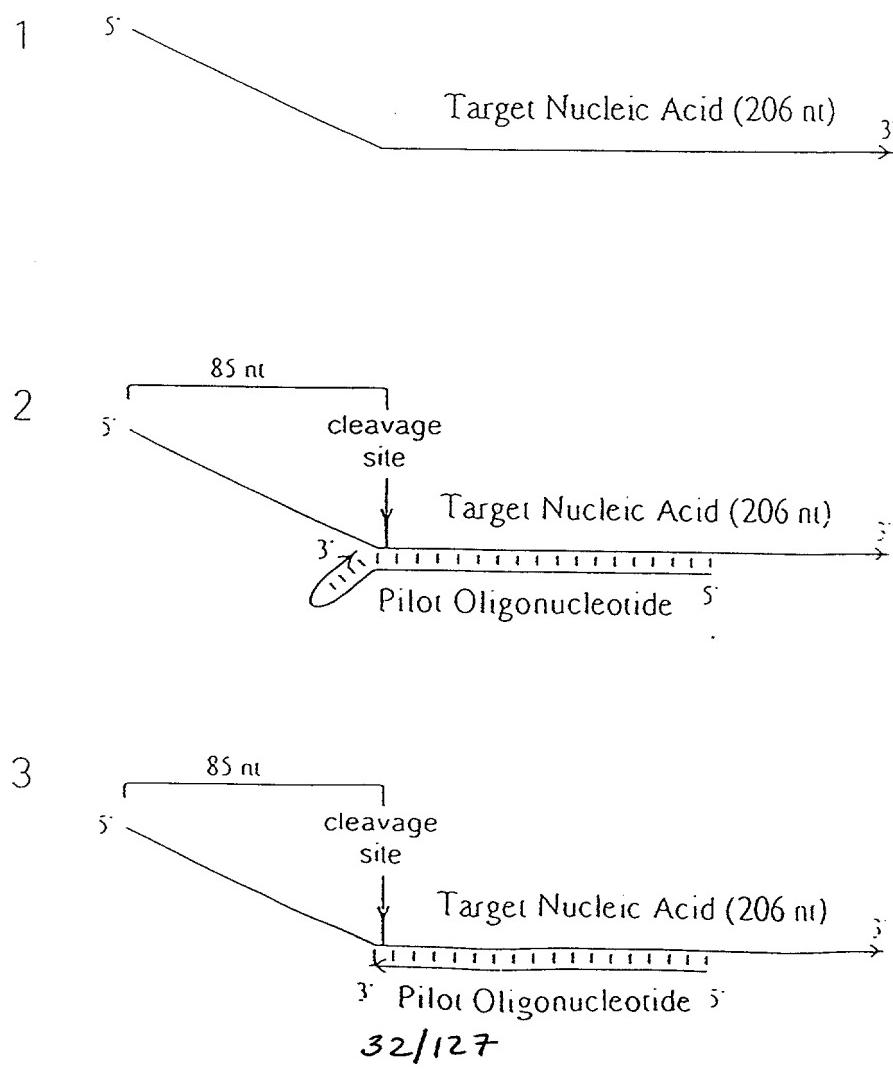
THE JOURNAL OF CLIMATE

FIGURE 21



000000000000000000000000

FIGURE 22A



THE HISTORY OF THE CHURCH OF JESUS CHRIST

FIGURE 22B

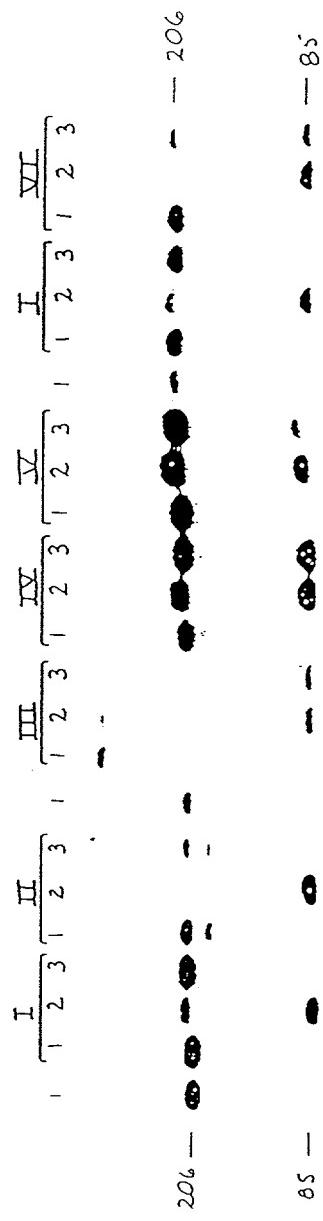
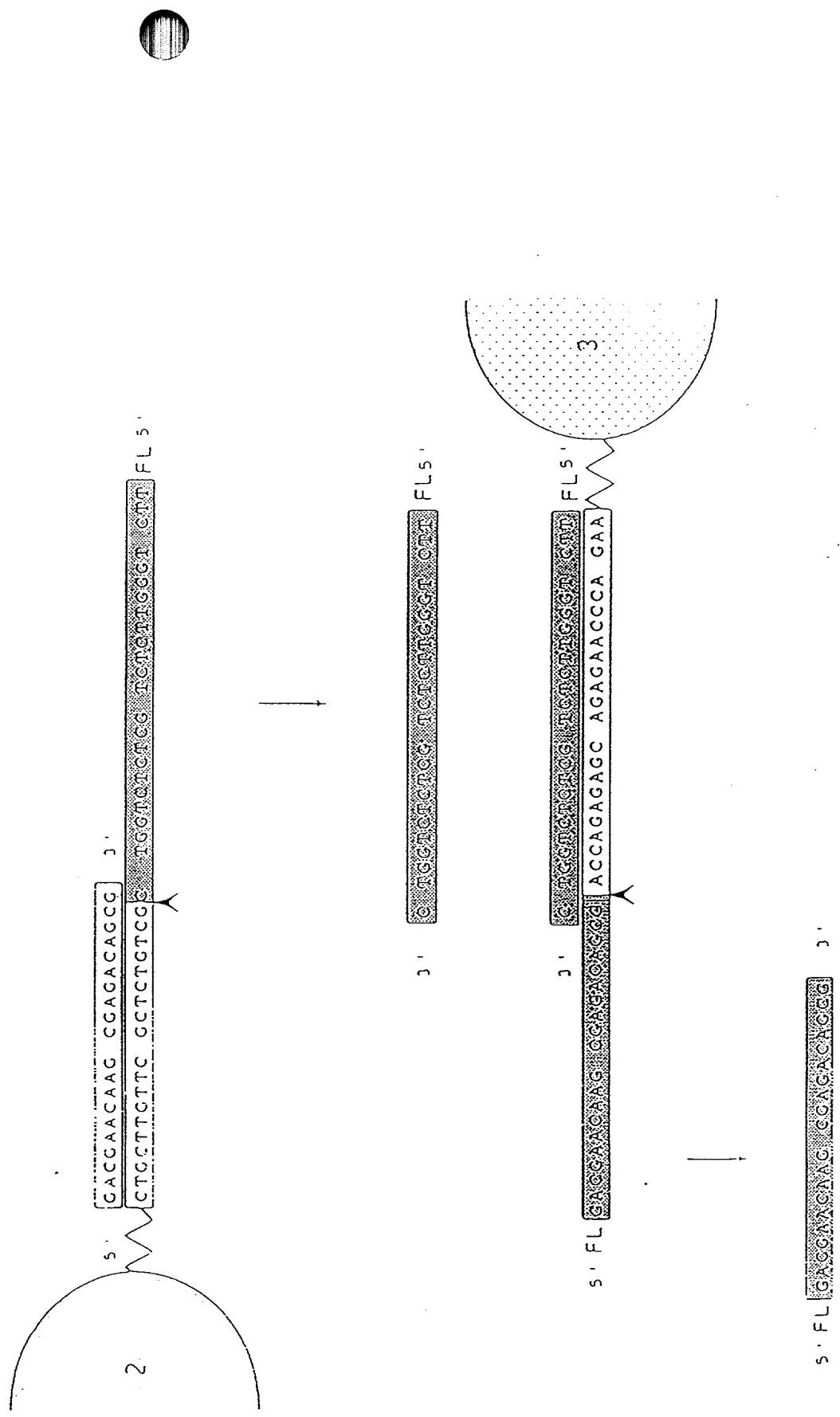


FIGURE 23



34/127

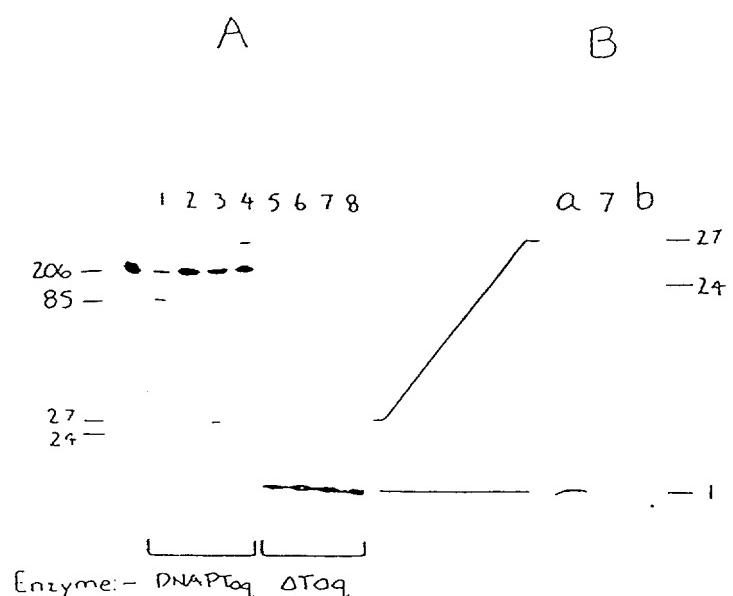
FIGURE 24

CDR Serial
Print
Classification

T T T A A A
- + - + + -
M M - + + + - M M

35/127

FIGURE 25

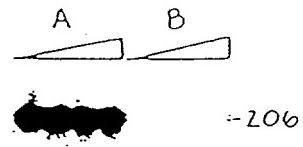
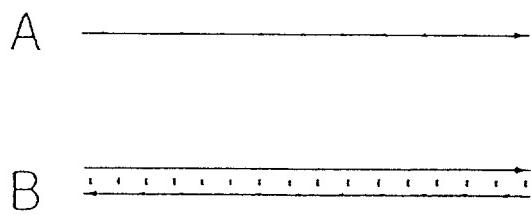


$\bullet \rightarrow p_i$

36 / 127

000000000000000000000000

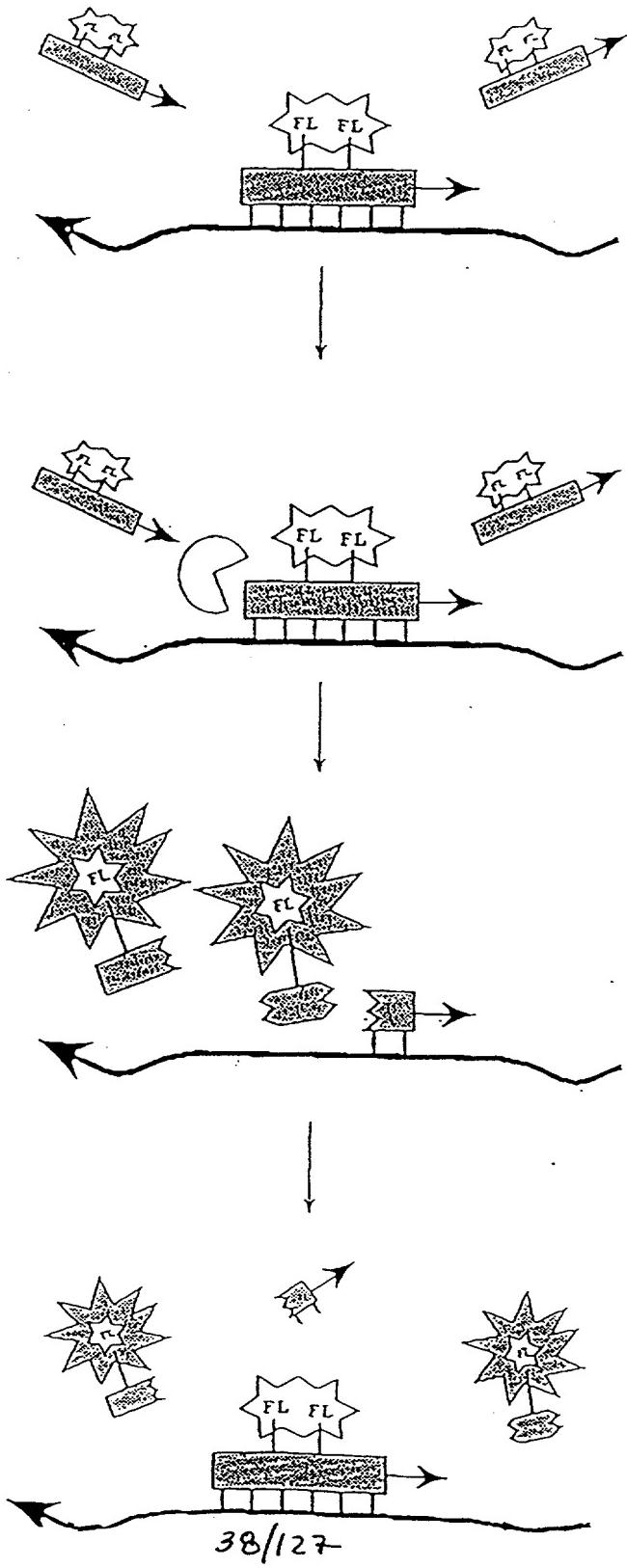
FIGURE 26



$=^{32}\text{P}$

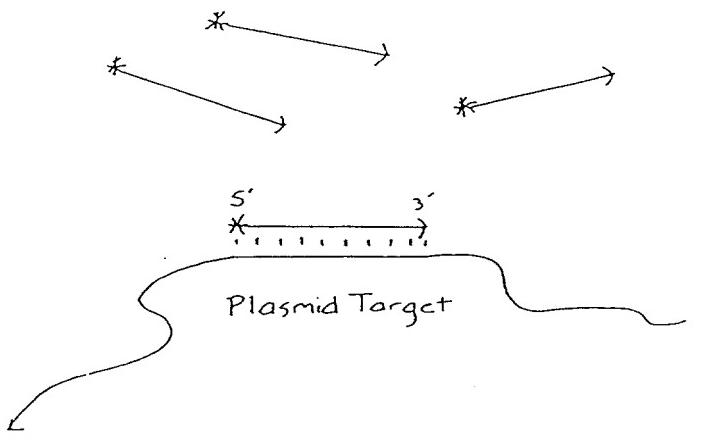
37/127

FIGURE 27



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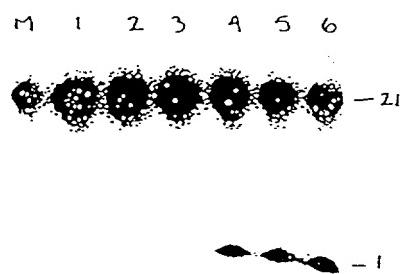
FIGURE 28A



* = ^{32}P 5' terminal phosphate

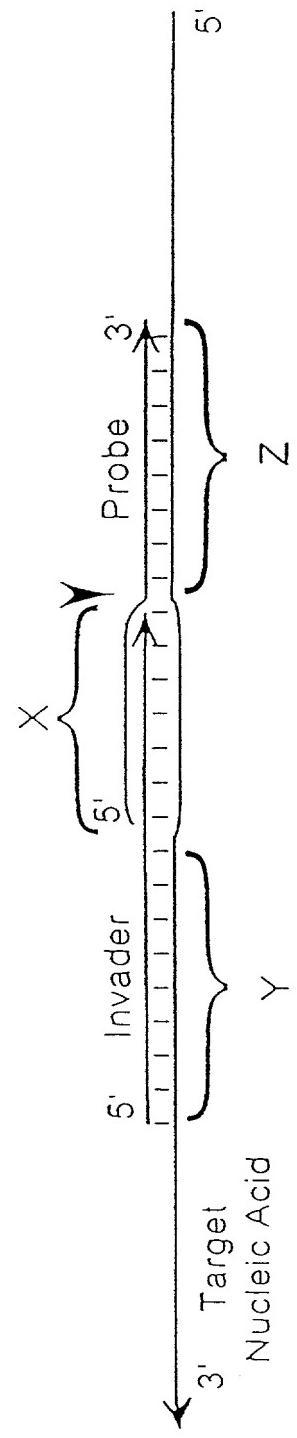
000000000000000000000000

FIGURE 28B



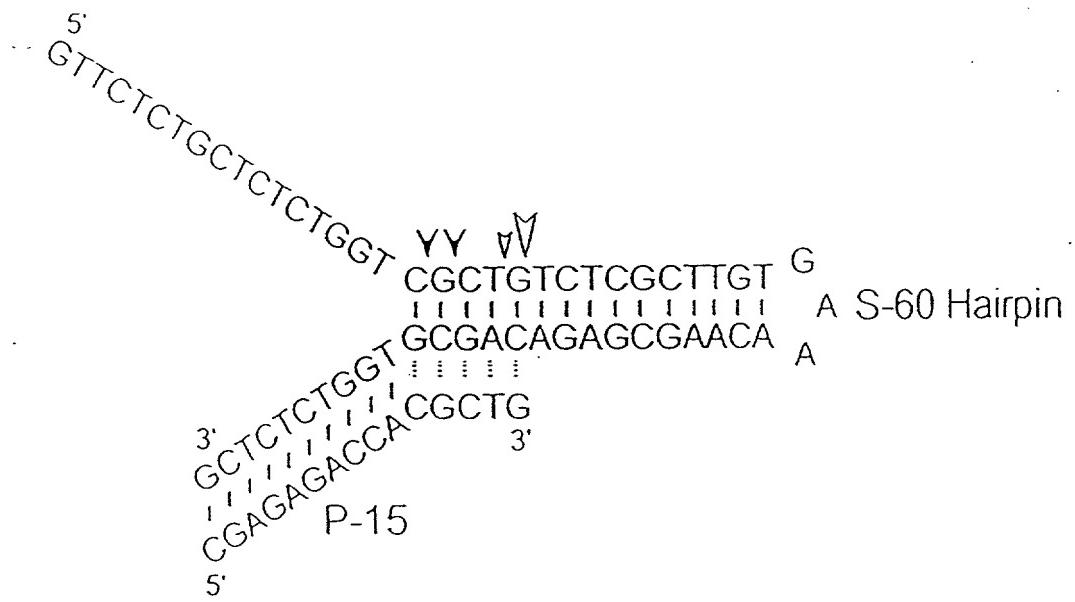
40/127

FIGURE 29



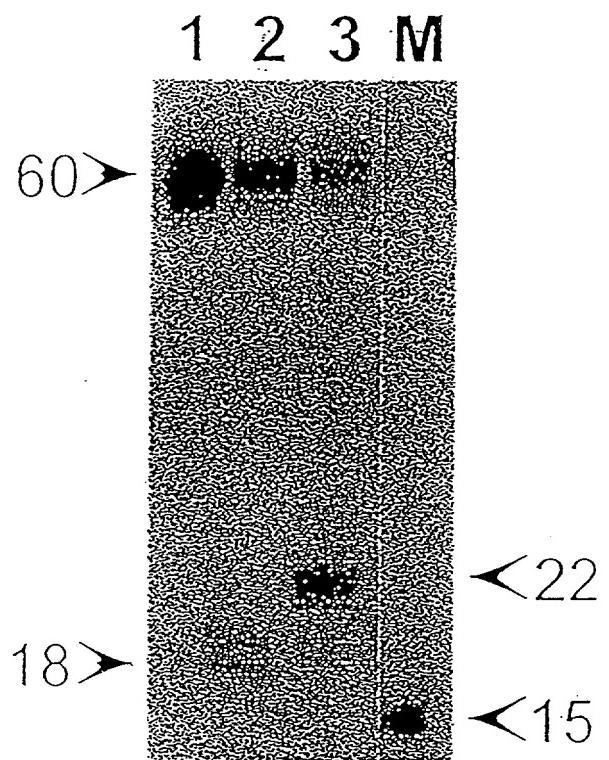
41/127

FIGURE 30



42/127

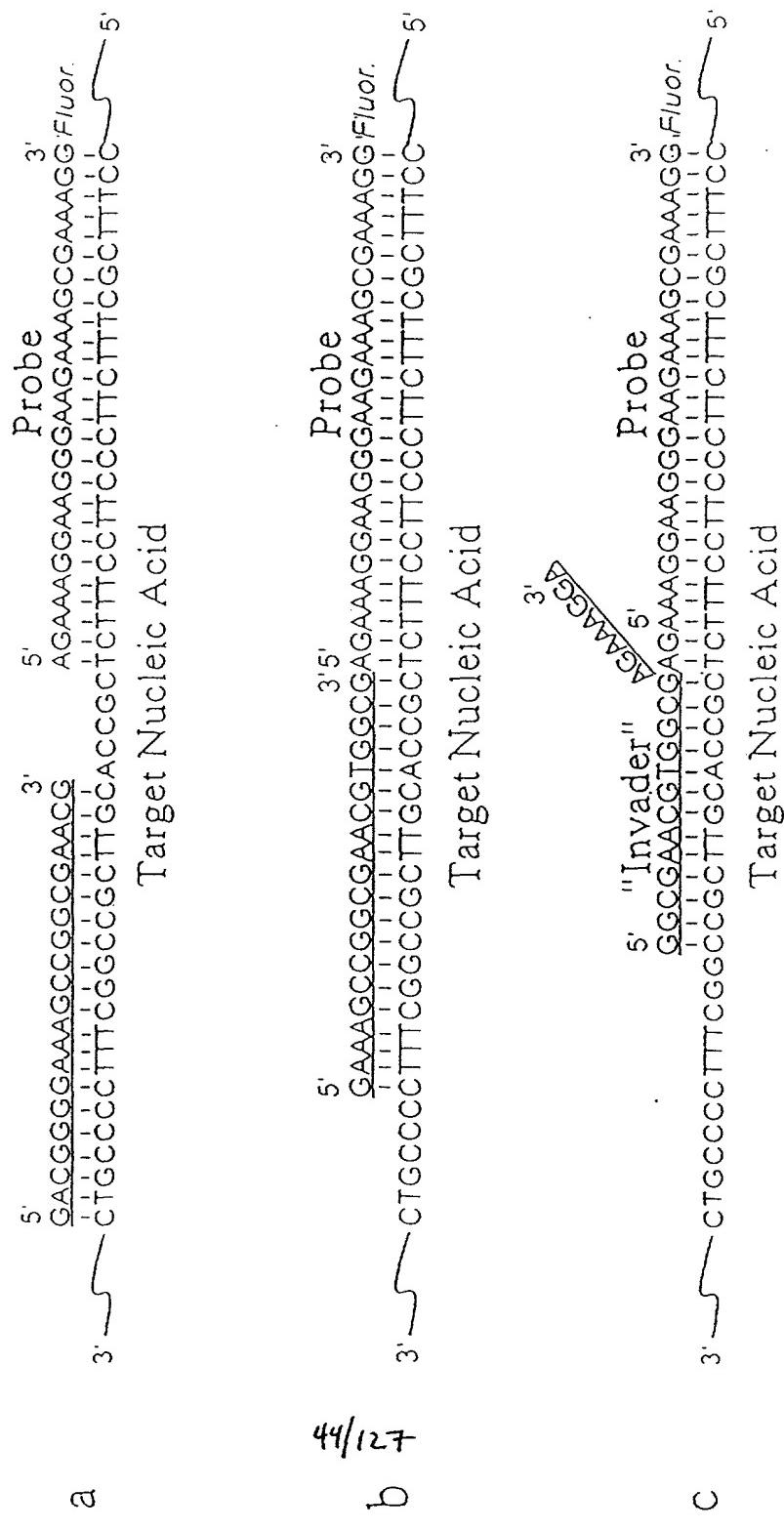
FIGURE 31



43/127

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FIGURE 32



10000000000000000000000000000000

8

7

6

5

4

3

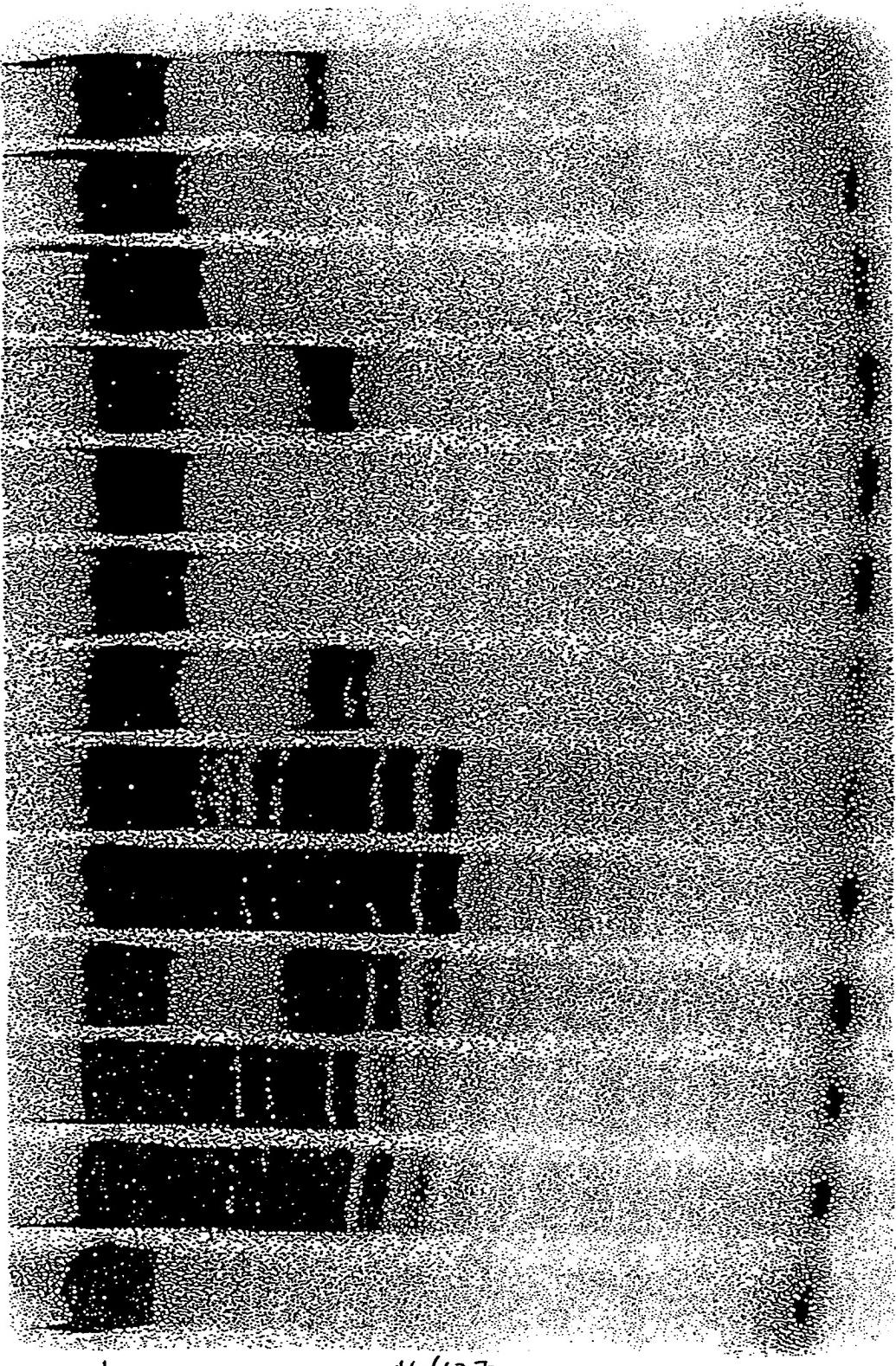
2

1

10000000000000000000000000000000

45/127

FIGURE 34

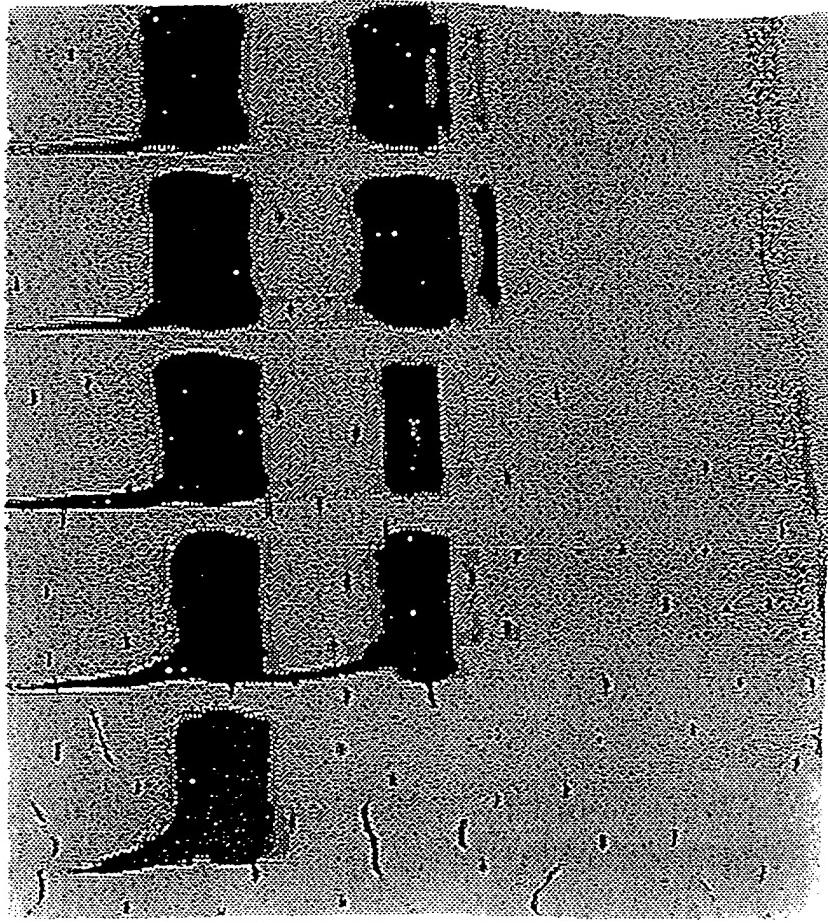


1

46/127

FIGURE 35 FIGURE 36

1 2 3 4 5



26 A

47/127

FIGURE 36

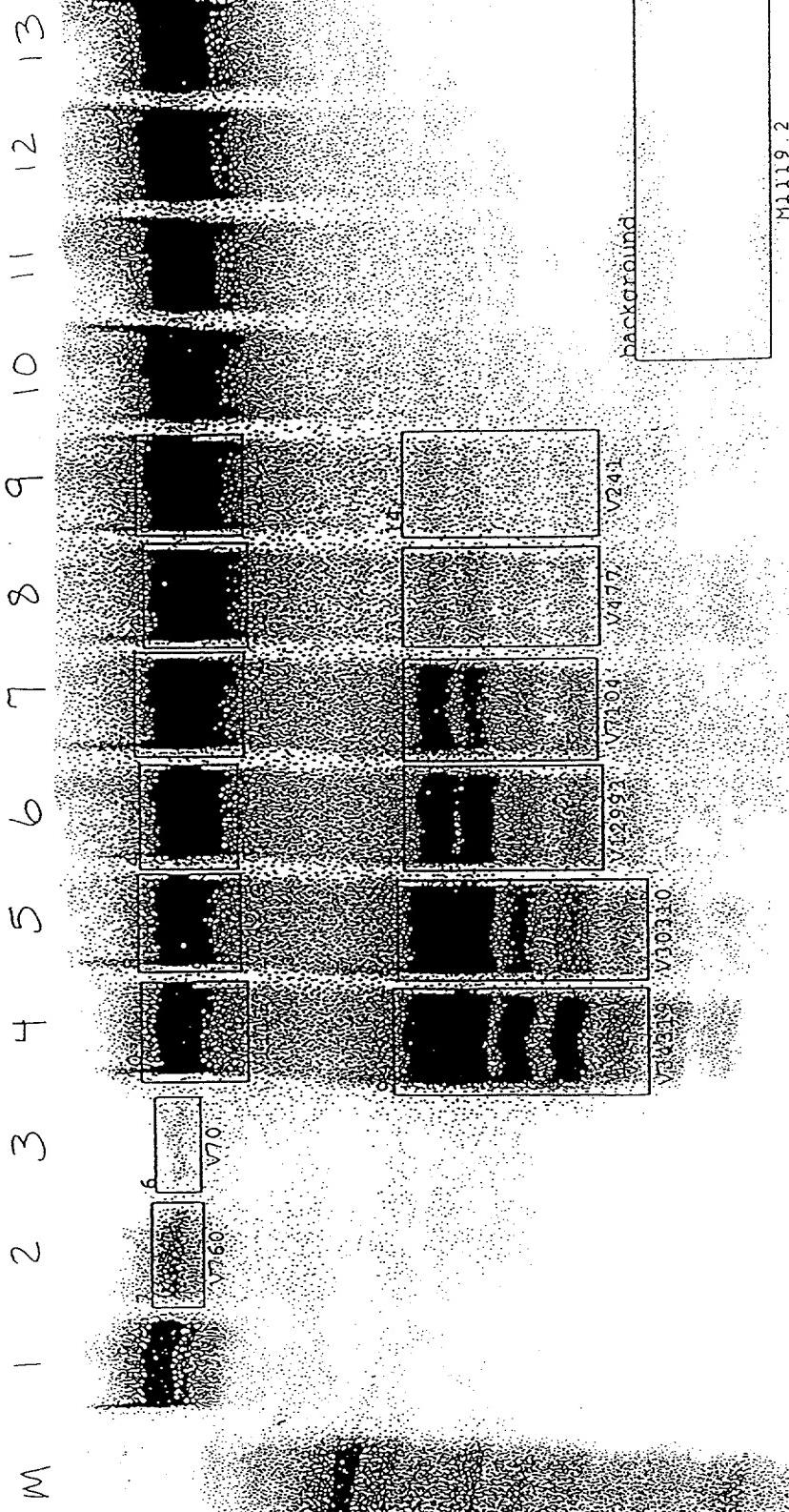


FIGURE 35. Frame 0

1 2 3 4 5 6 7 8 9 10 11

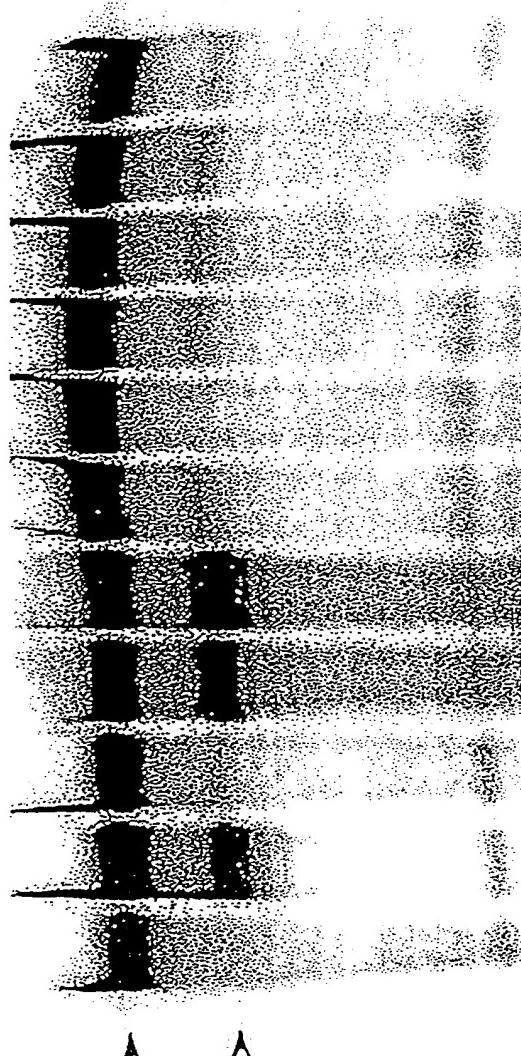
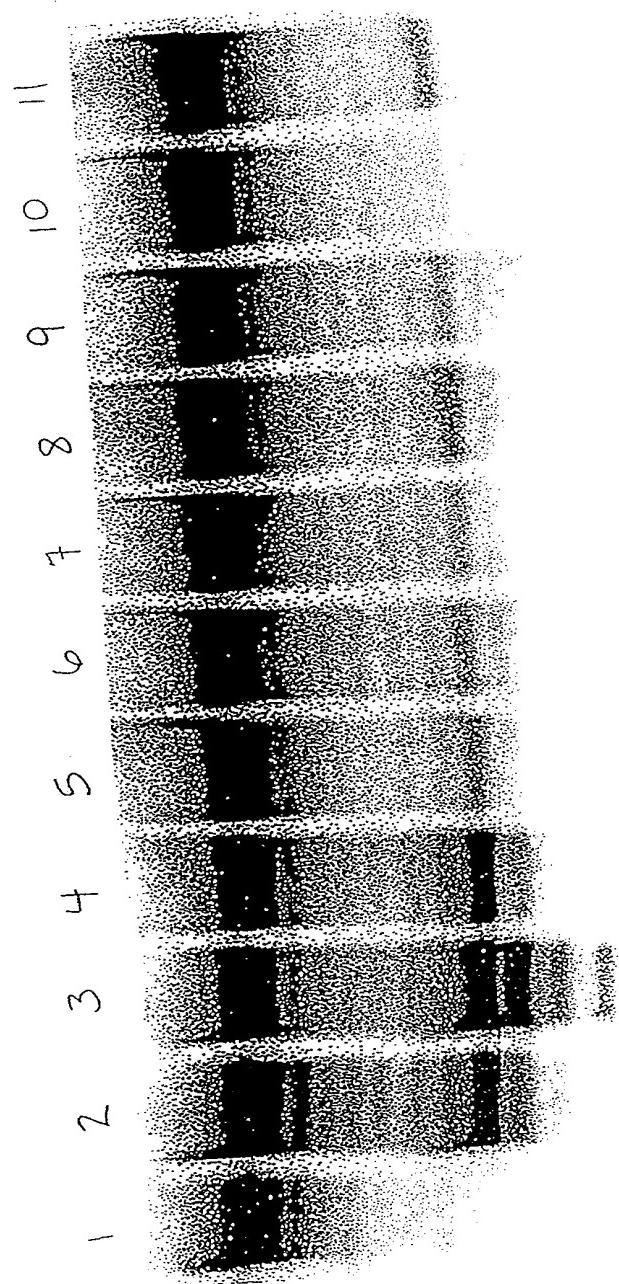


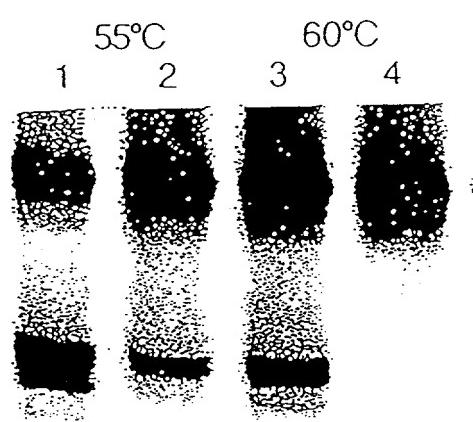
FIGURE 38



0146 66 44 77 88 99 00 11 22 33 44 55 66 77 88 99 00



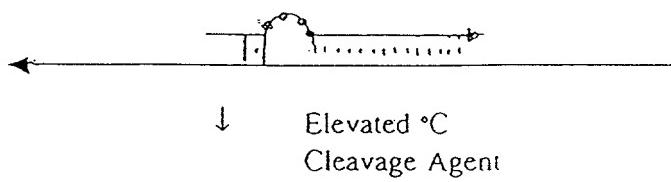
FIGURE 39



51/127

FIGURE 40

a.



b.

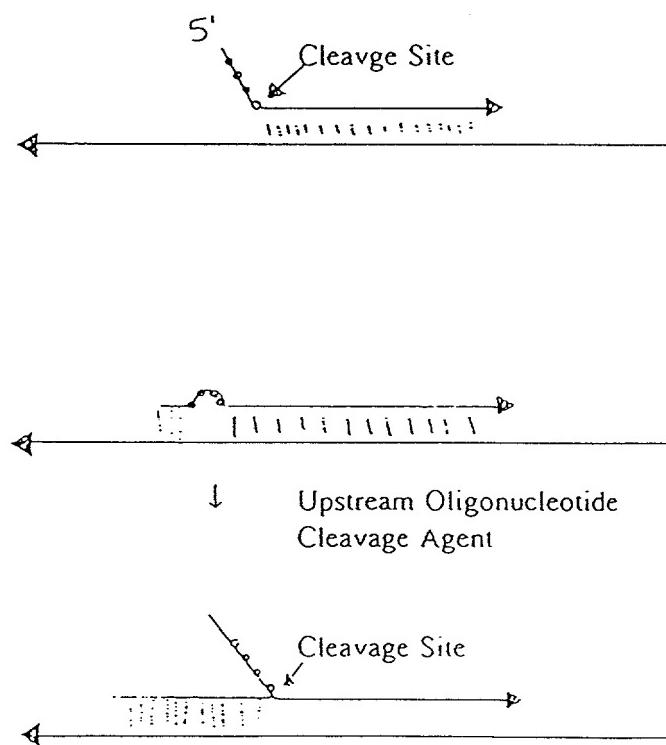
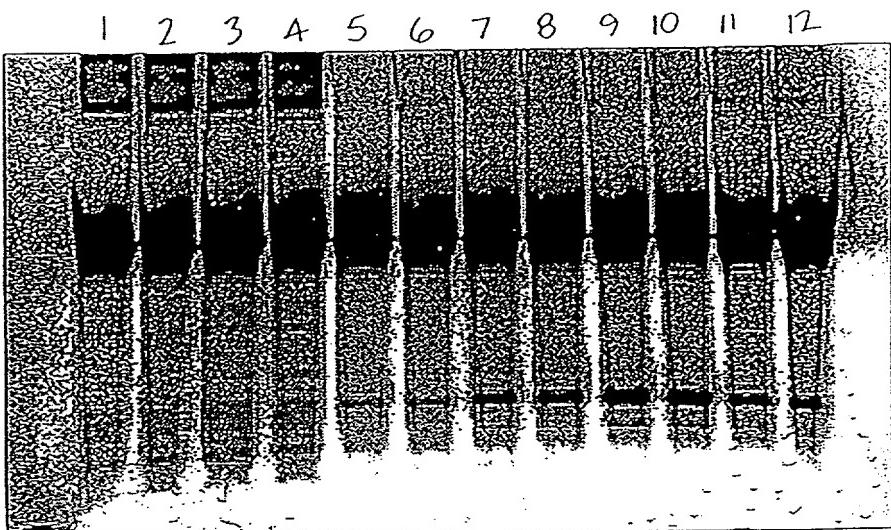


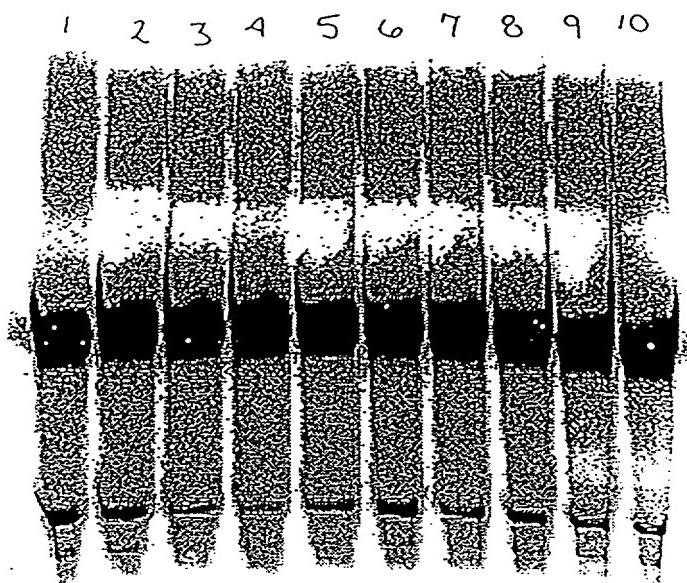
FIGURE 41

FIGURE 42



54/127

FIGURE 43



09684305 11070000

55/127

FIGURE 44

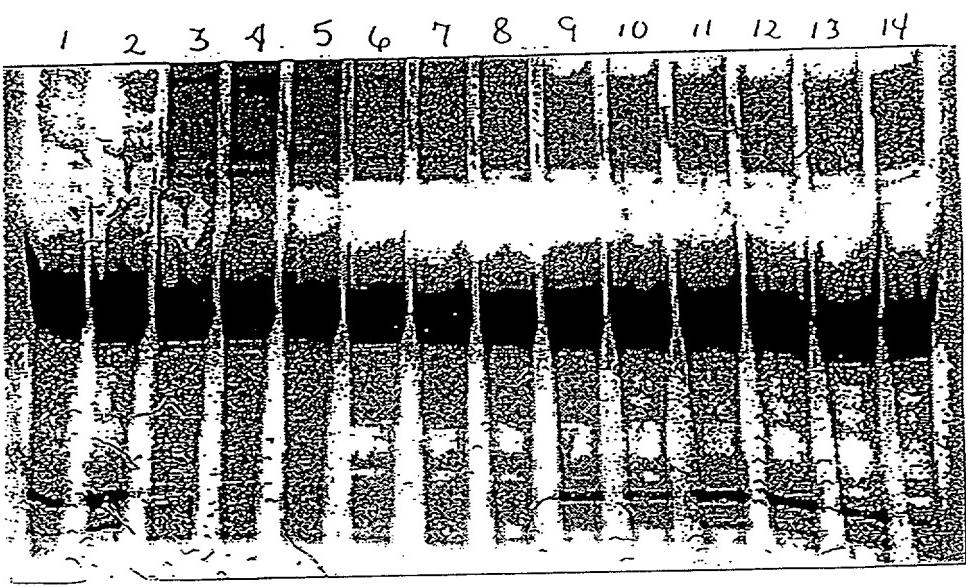
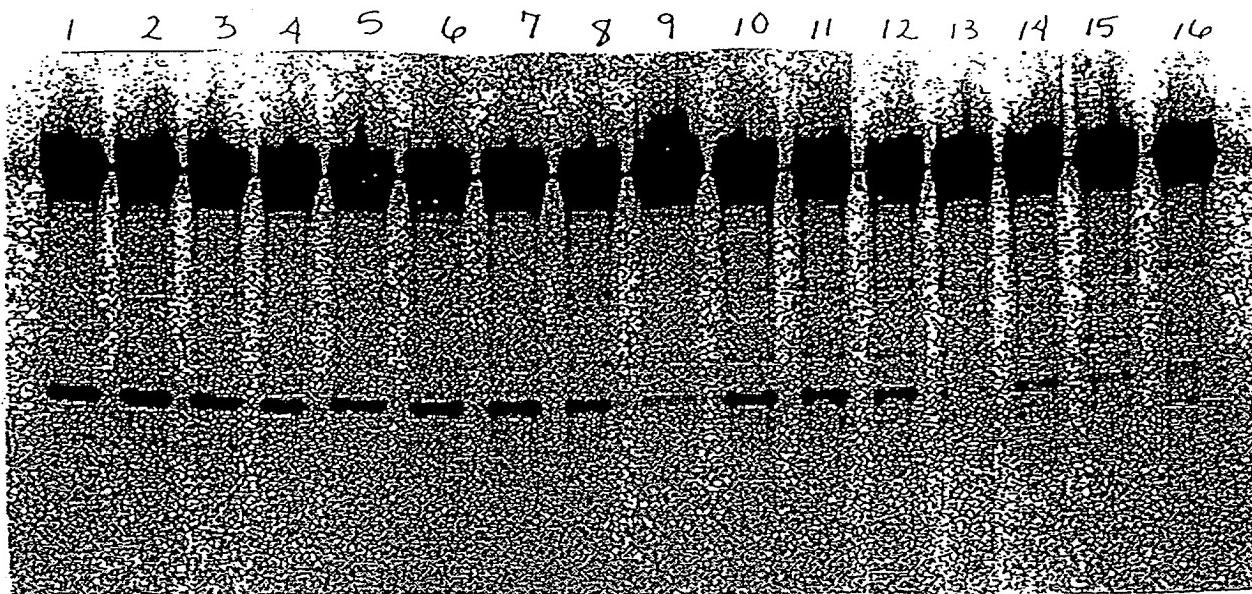


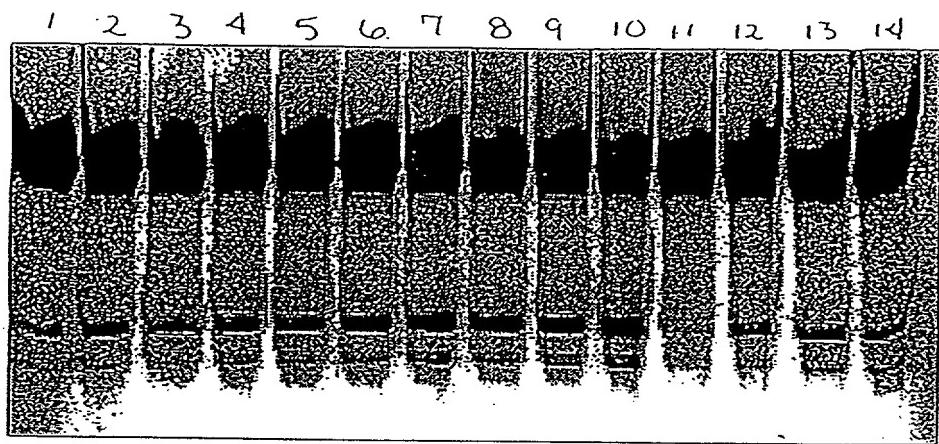
FIGURE 45



095843056 410000000

57/127

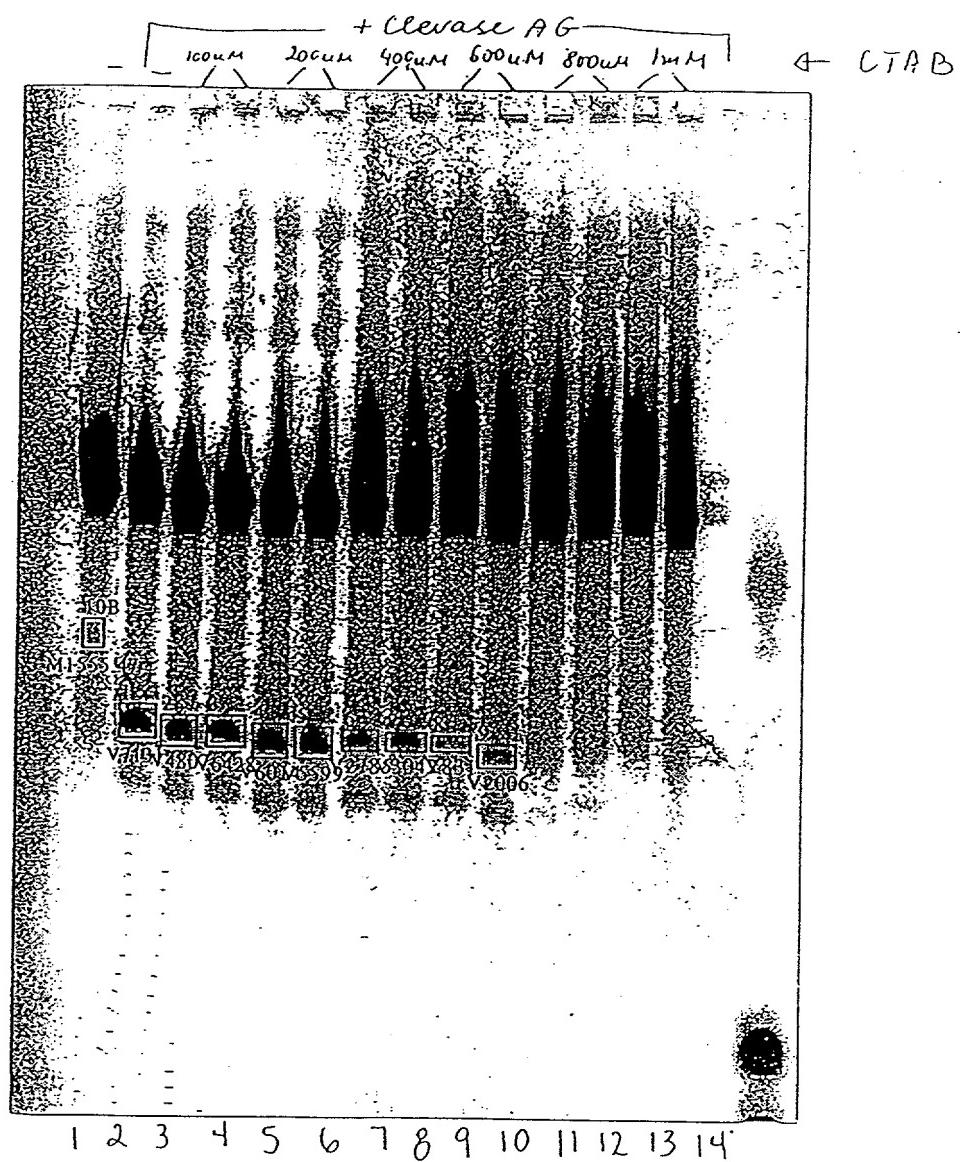
FIGURE 46



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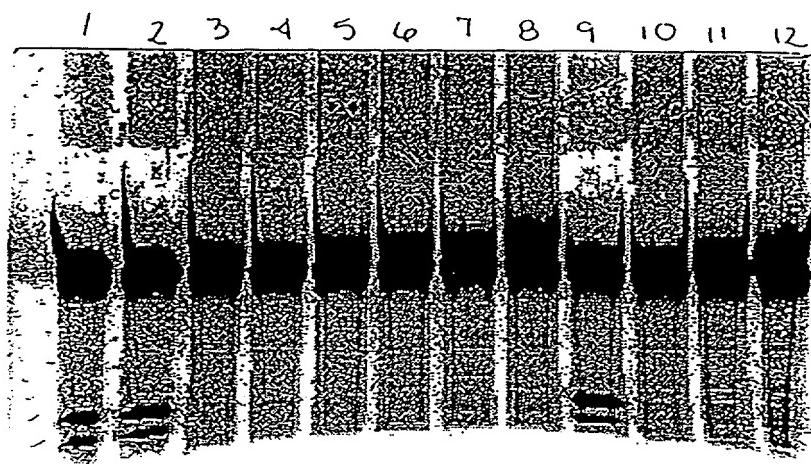
58/127

FIGURE 47



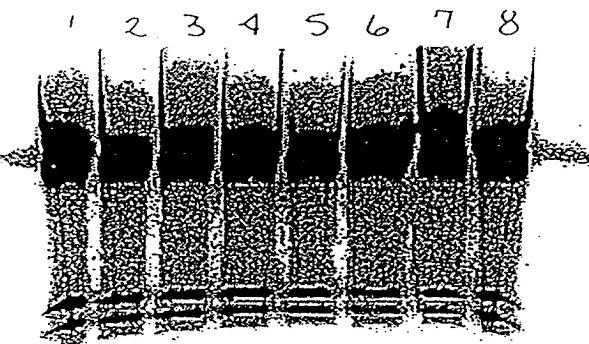
59/127

FIGURE 48



60/127

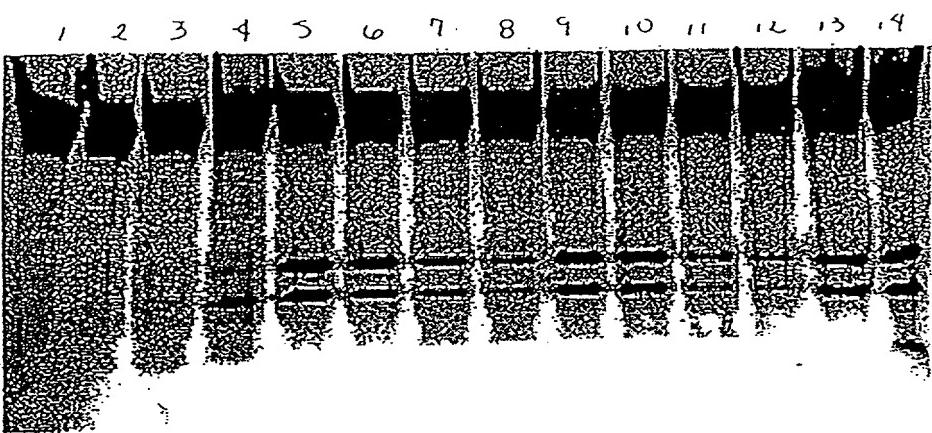
FIGURE 49



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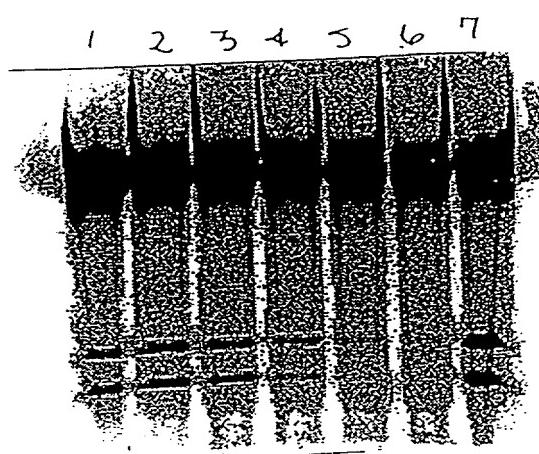
61 / 127

FIGURE 50



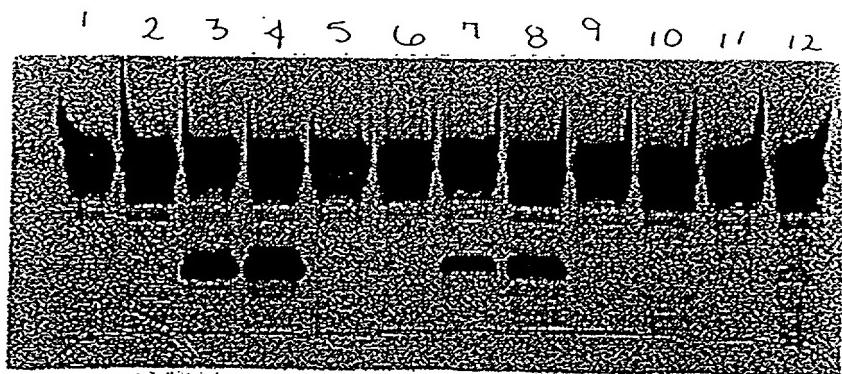
62/127

FIGURE 51



63/127

FIGURE 52



64/127

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FIGURE S3

a

— + AG Th

Target RNA

UNCLEAVED
Probe →

CLEAVED
Probe →

65/127

b

— + AG Th

1 2 3

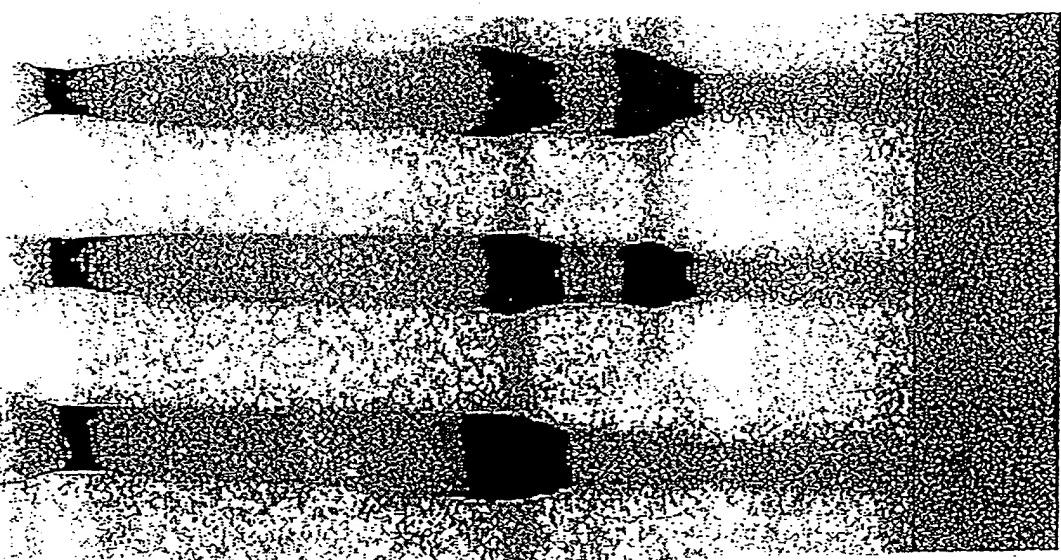
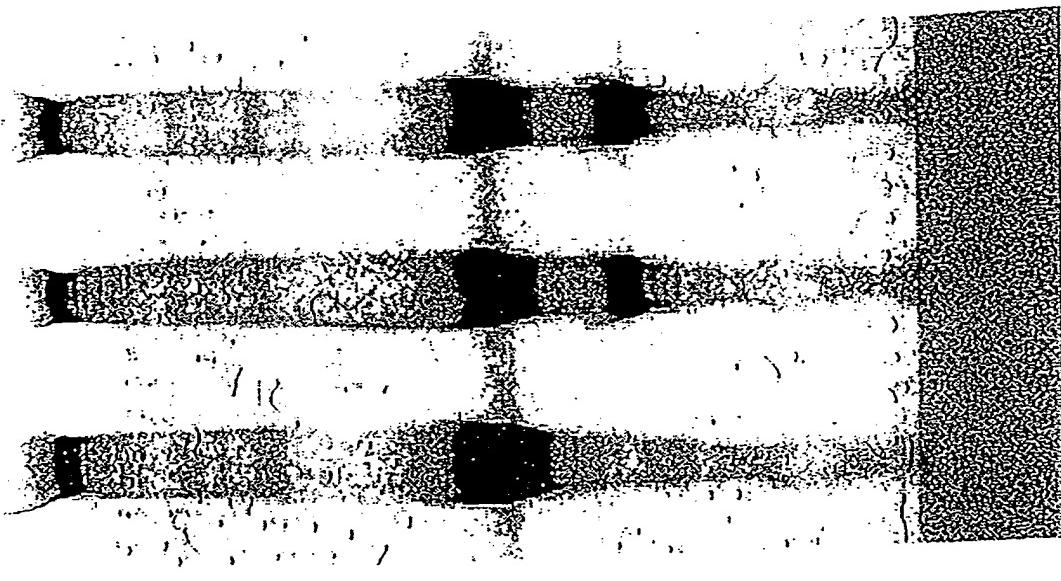


FIGURE 54

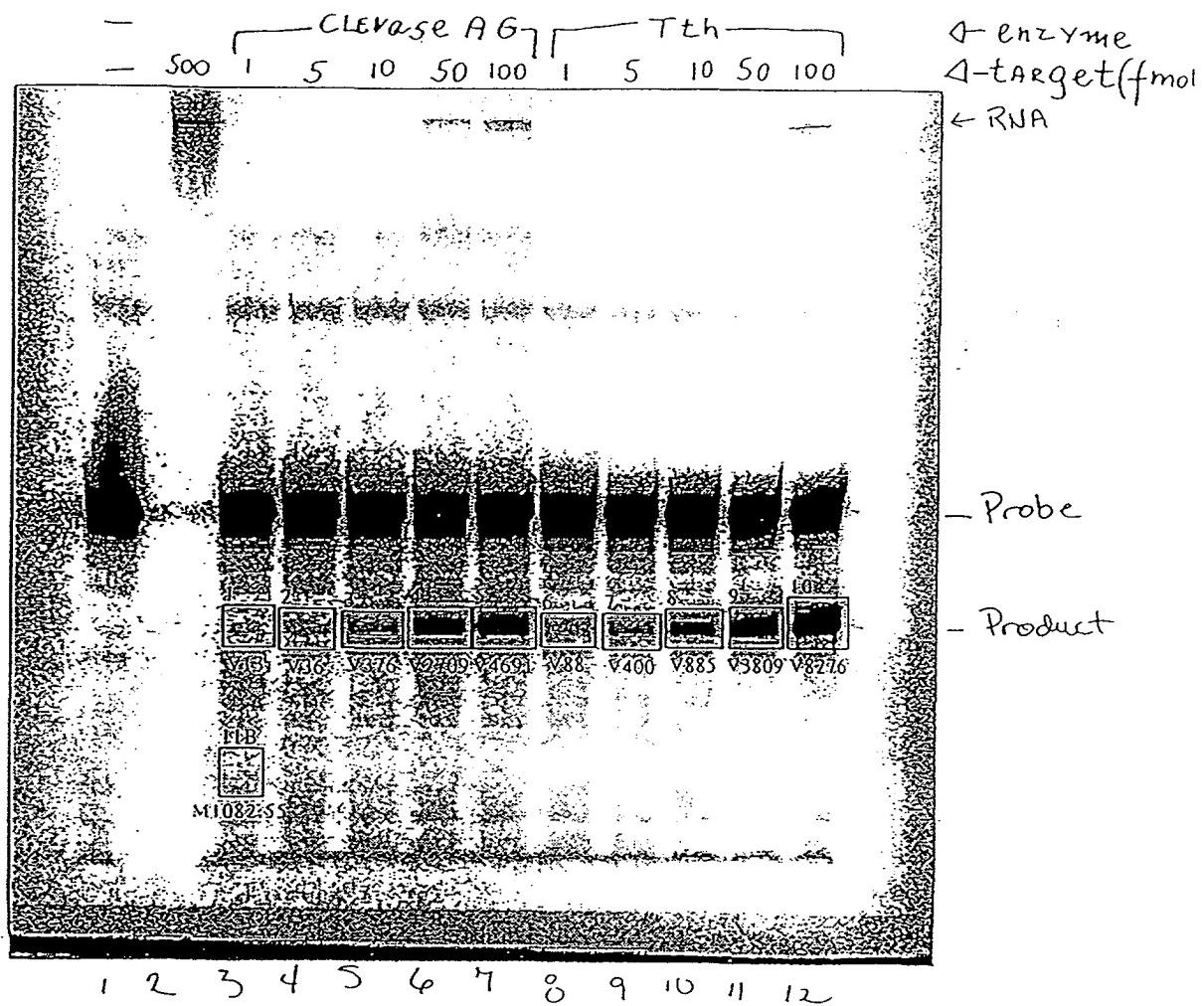
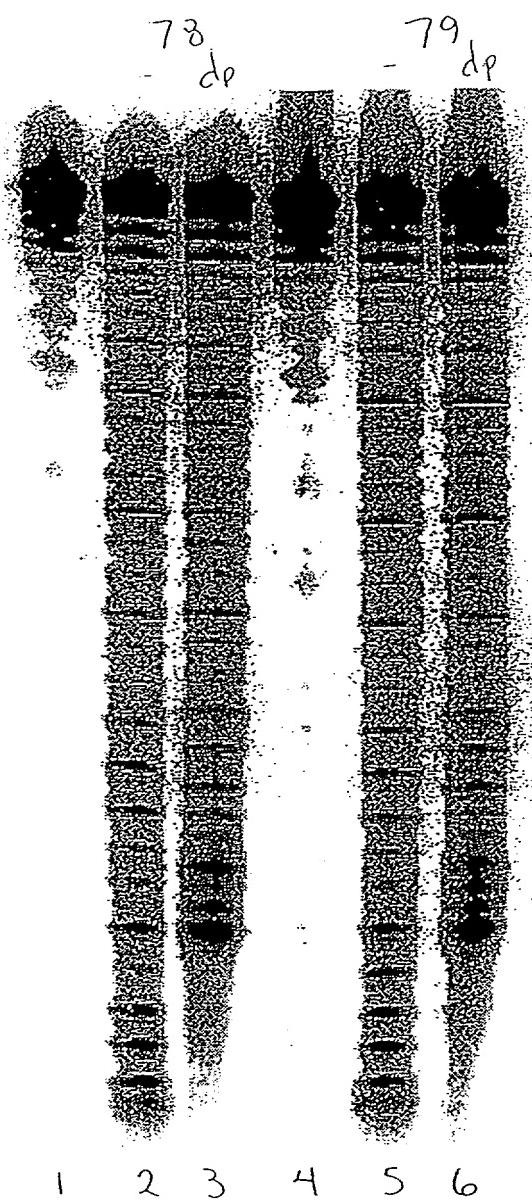


FIGURE 55



67/127

FIGURE 56

70 (C10 amino T's)
74 (C6 amino T's)

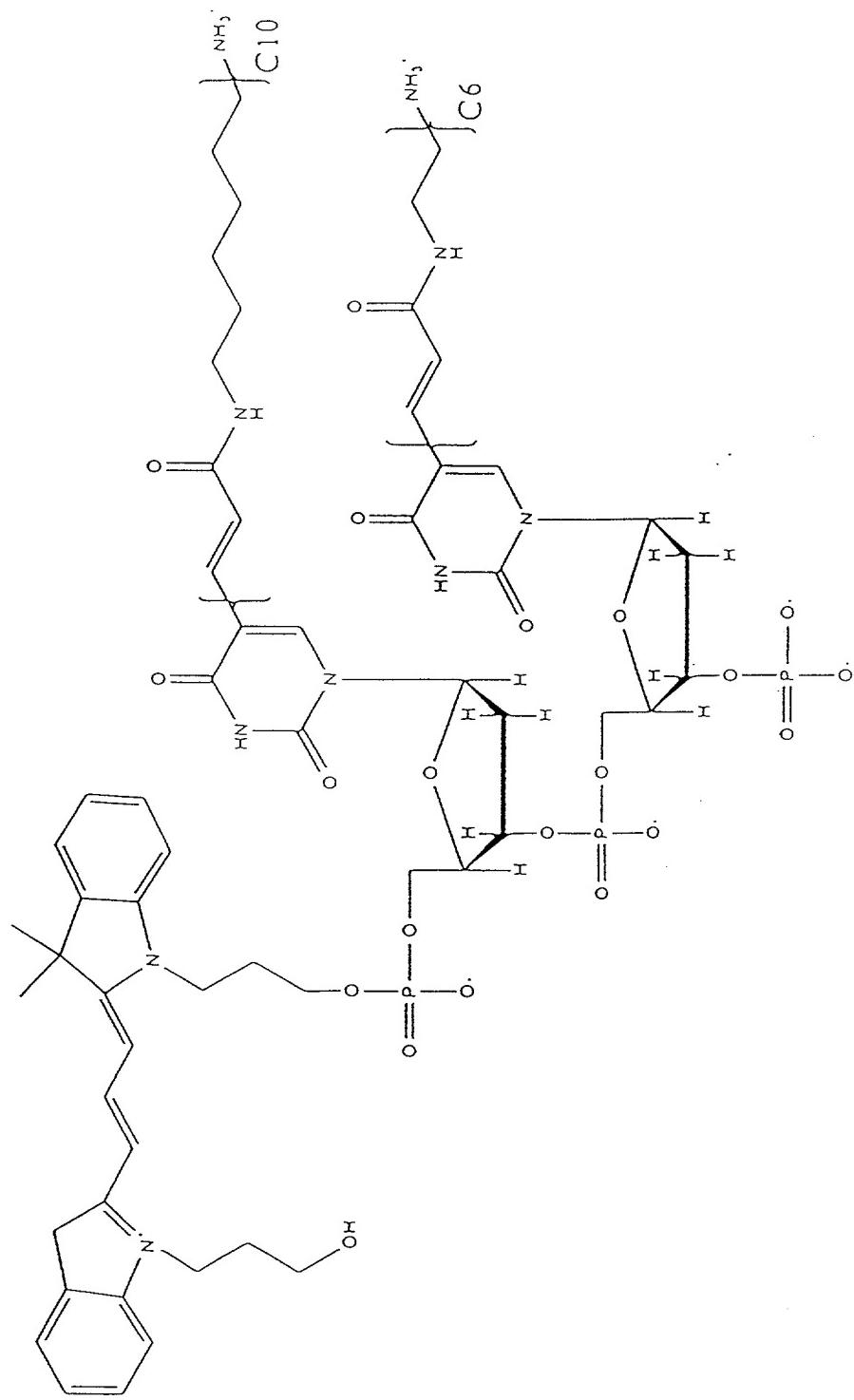
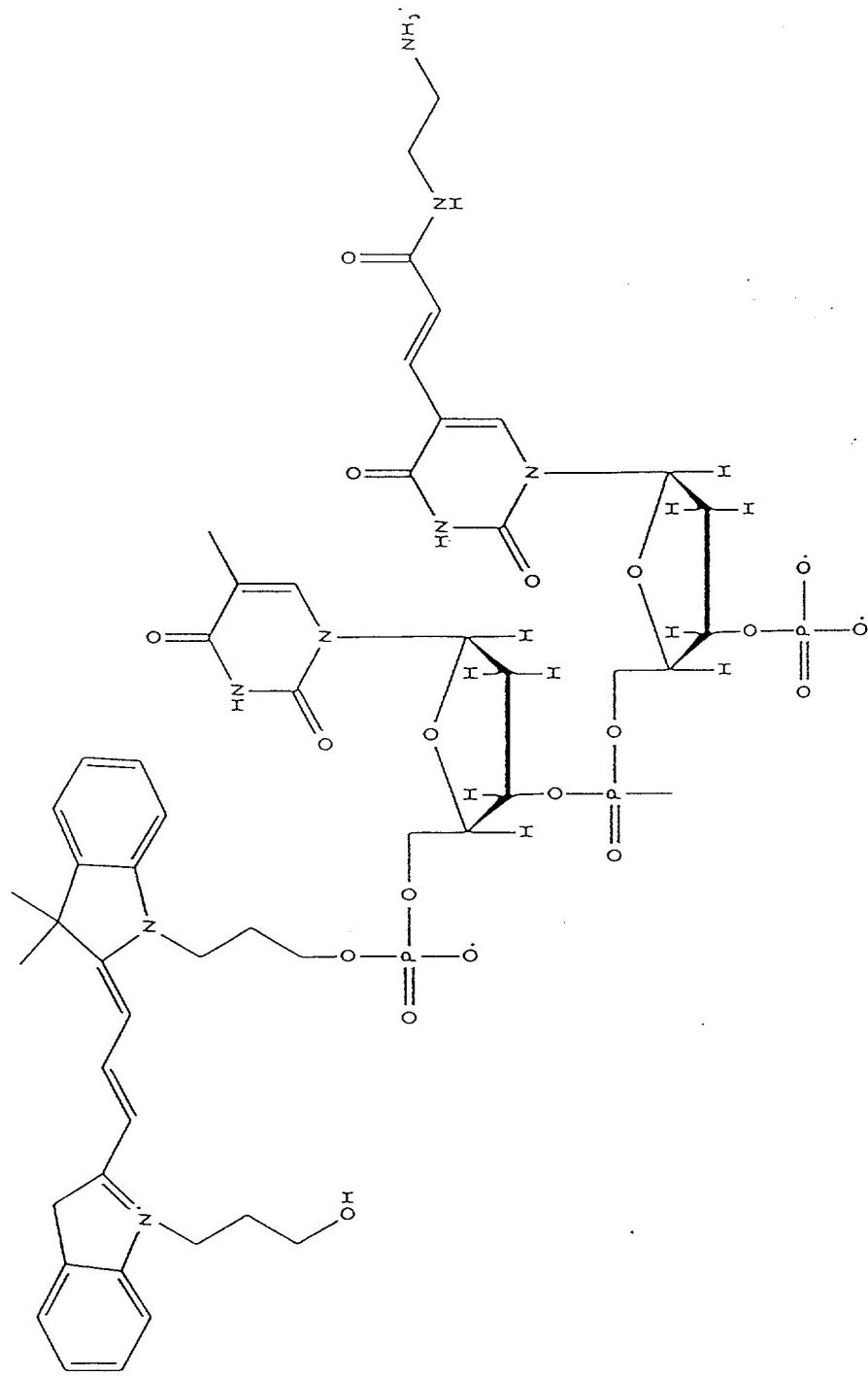


FIGURE 57

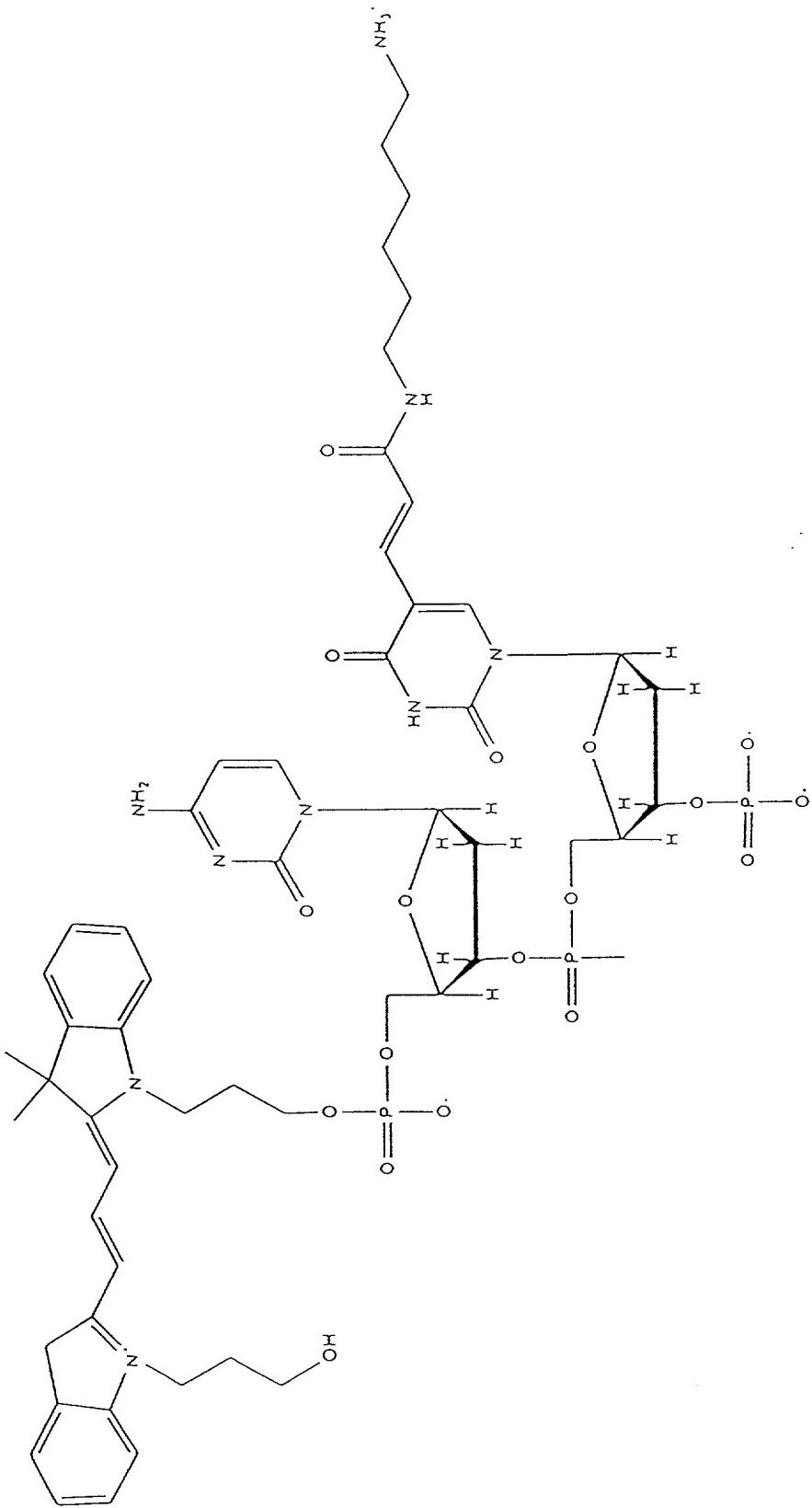
75



69/127

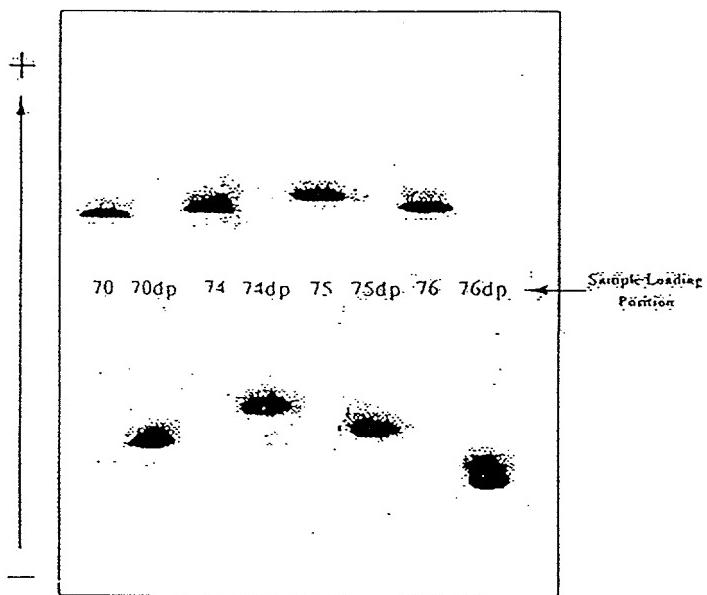
FIGURE 58

76



70/127

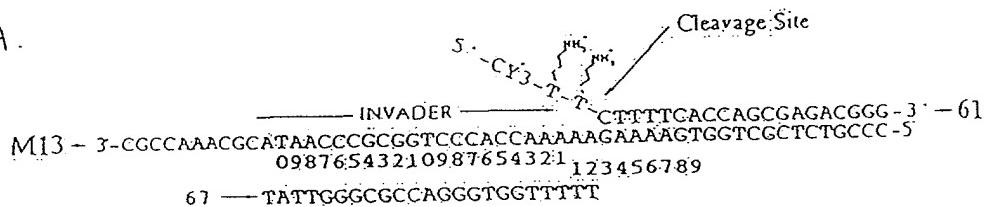
FIGURE 59



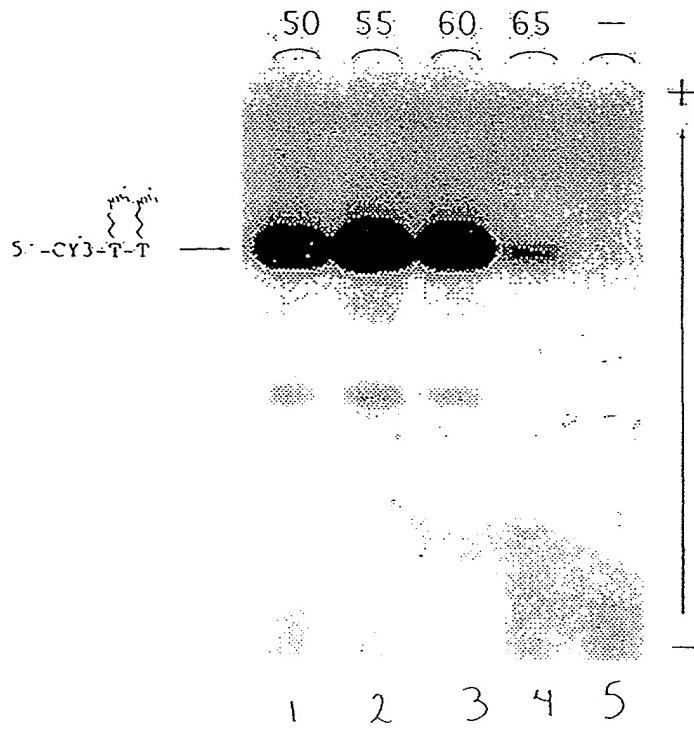
71/127

FIGURE 60

A.

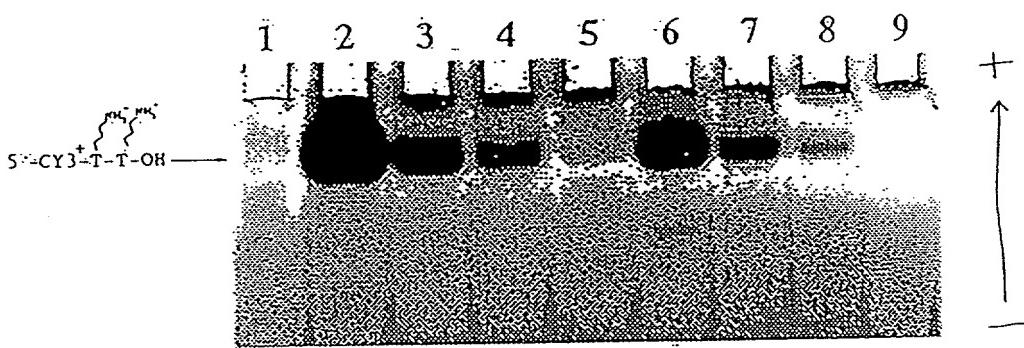


B.



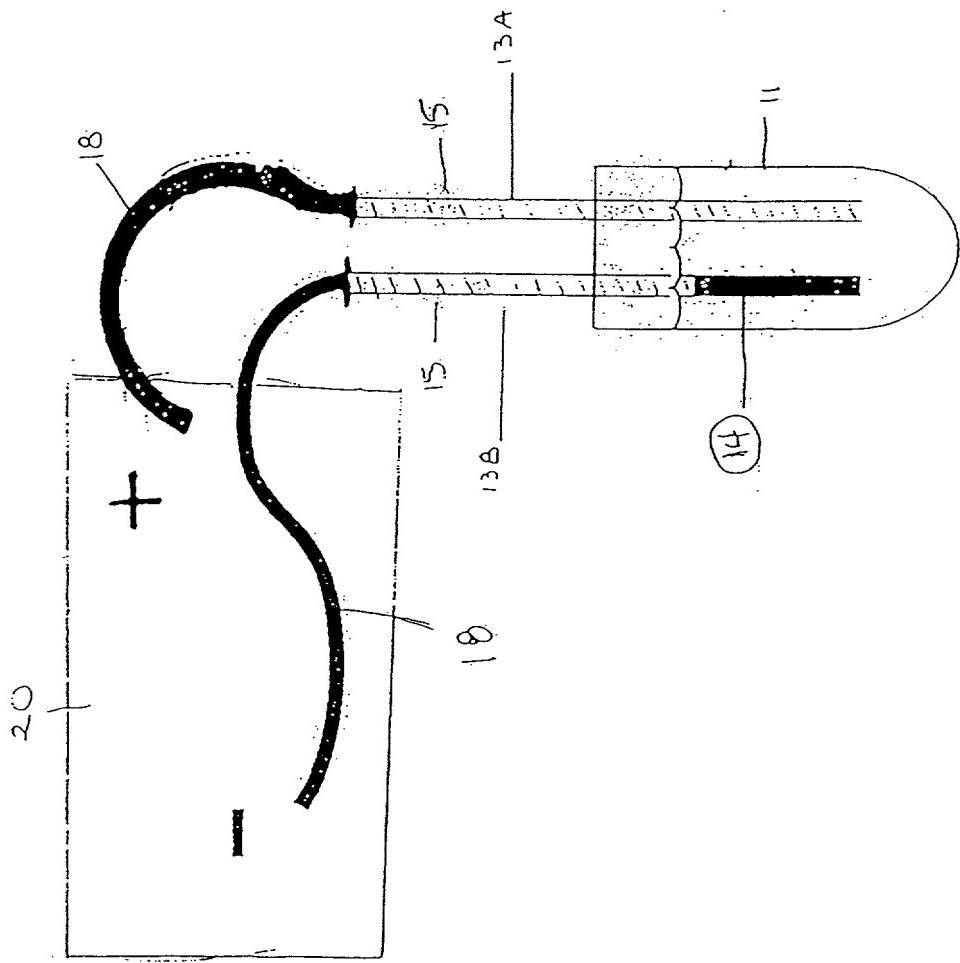
72/127

FIGURE 61



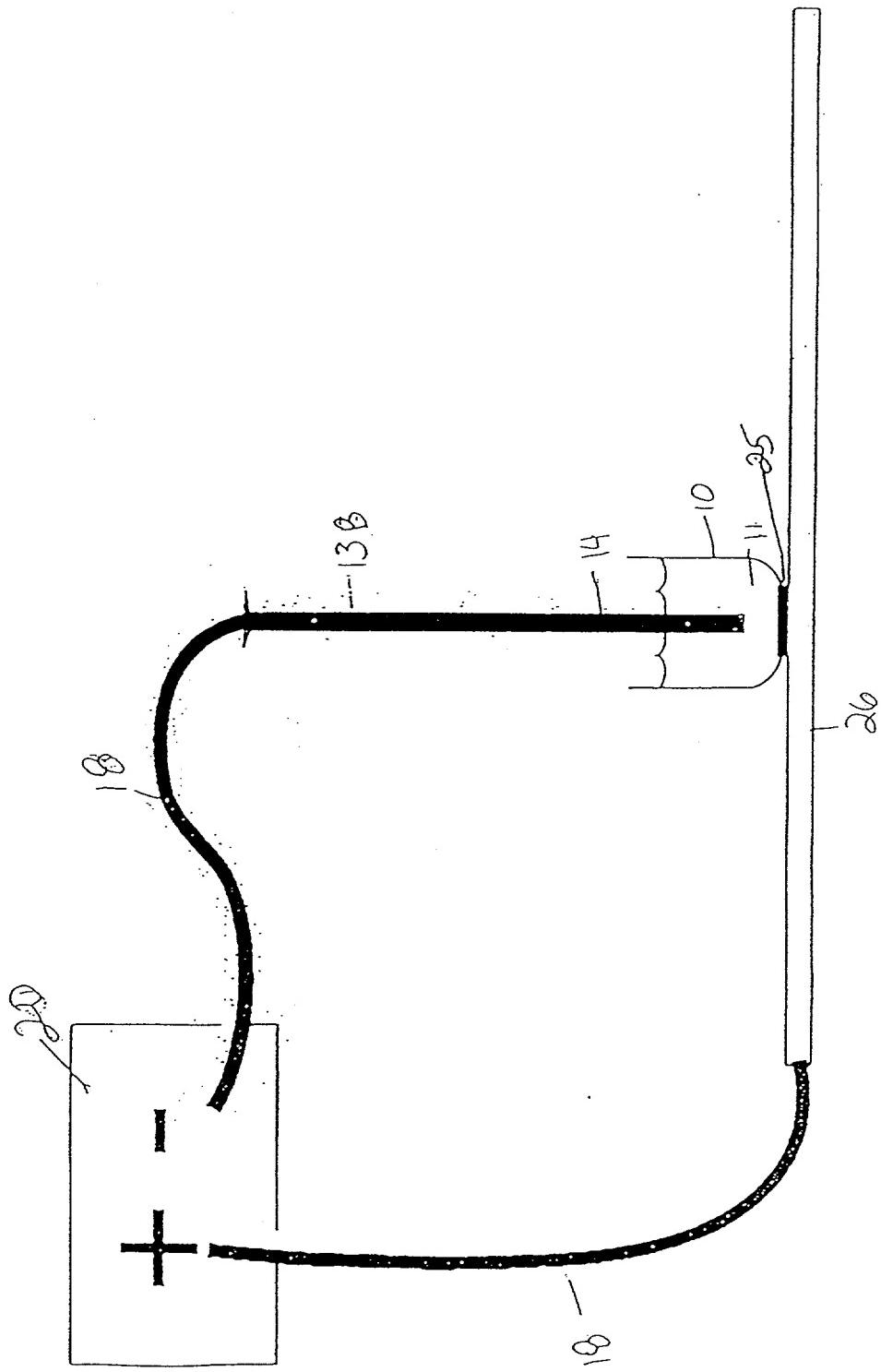
73/127

FIGURE 62



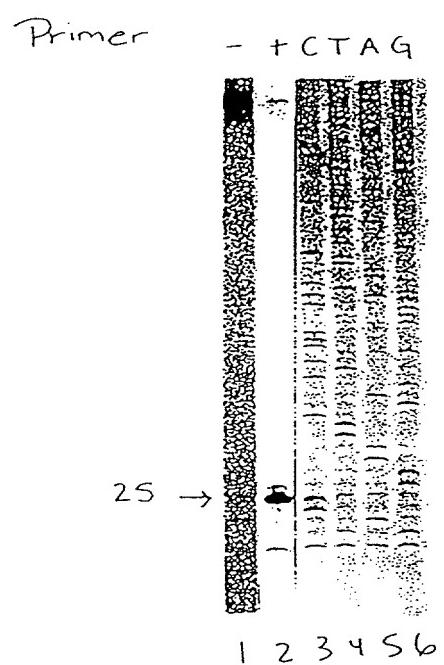
74/127

FIGURE 63



75/127

FIGURE 64



76/127

FIGURE 65

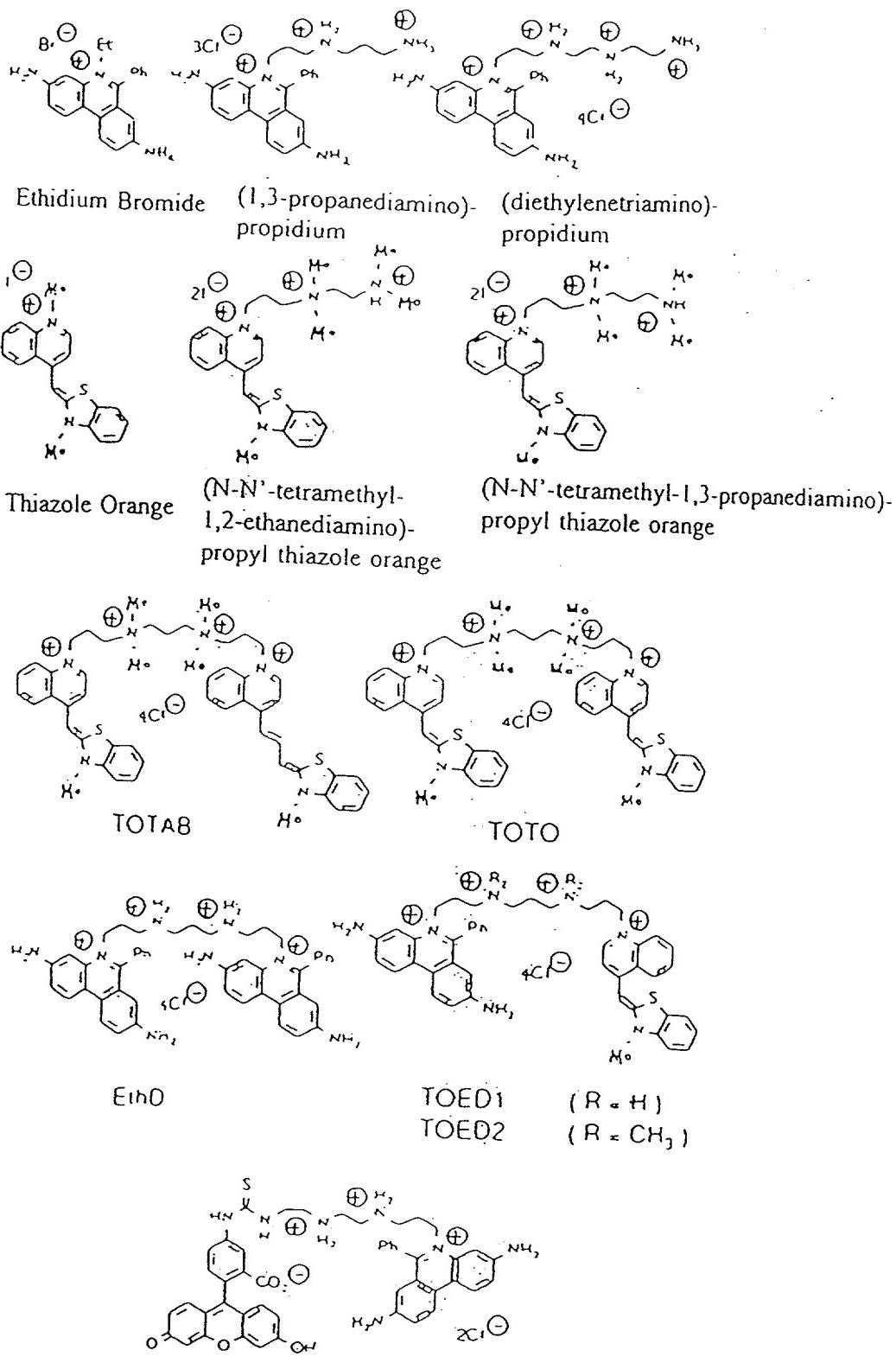
5' AGAAAGGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 a

5' CAG AAGGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 b

5' CAGGG V GGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 c

5' CAGGGTAC V AGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAGAAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTCCTCCCTTCTTCGCTTCC 5'
 d

FIGURE 66



78/127

FIGURE 67

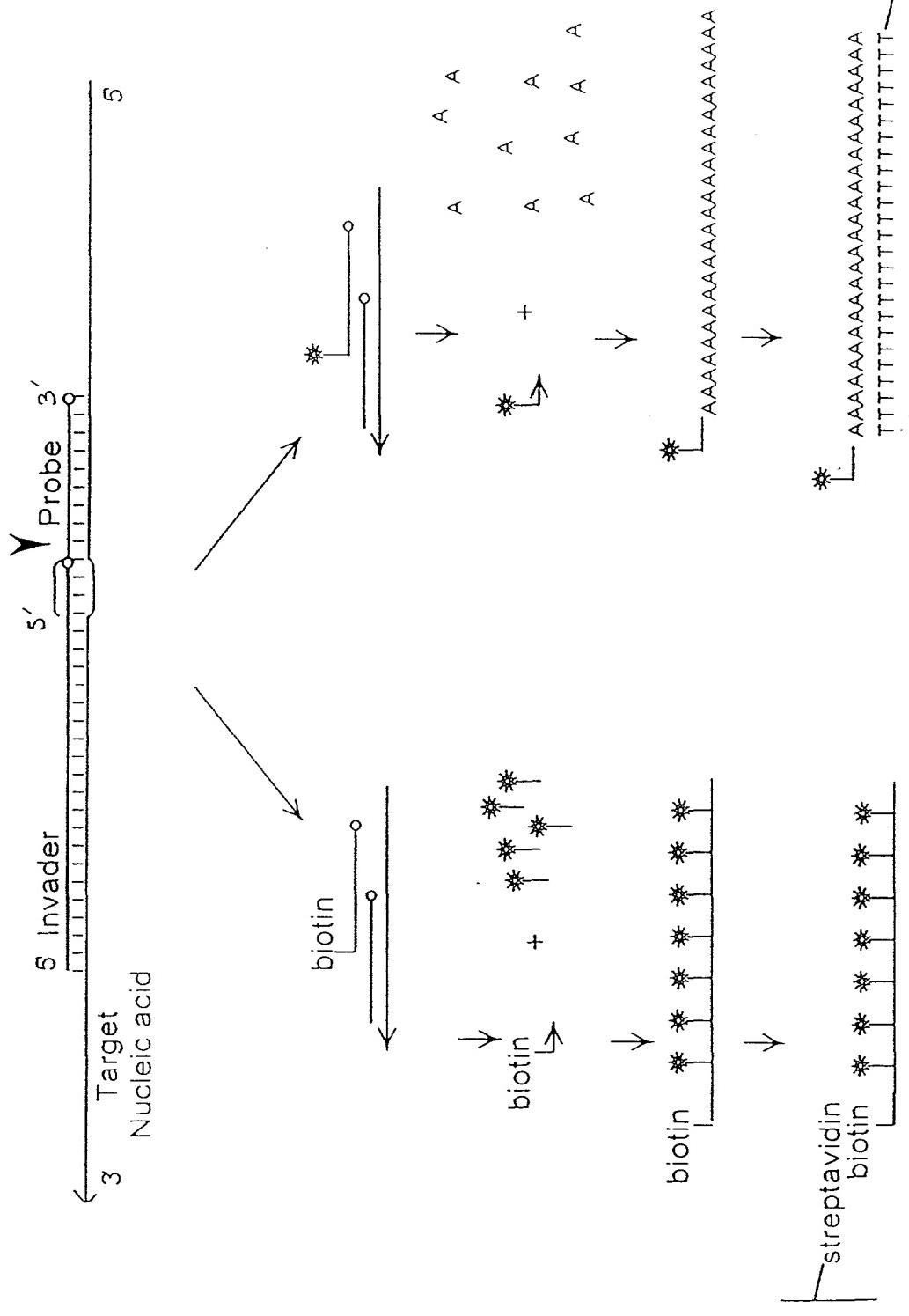


FIGURE 68

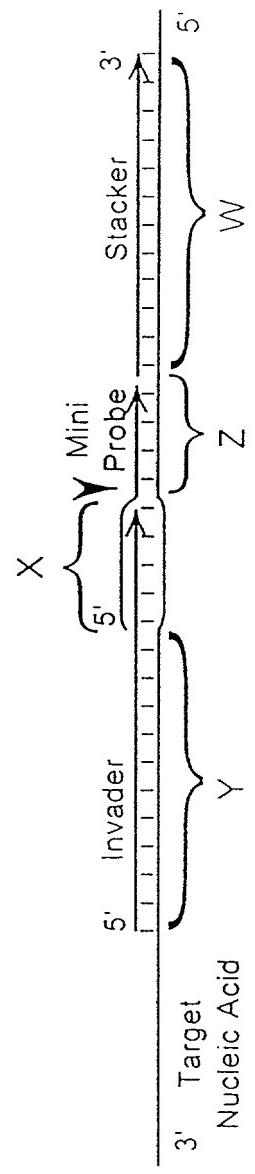
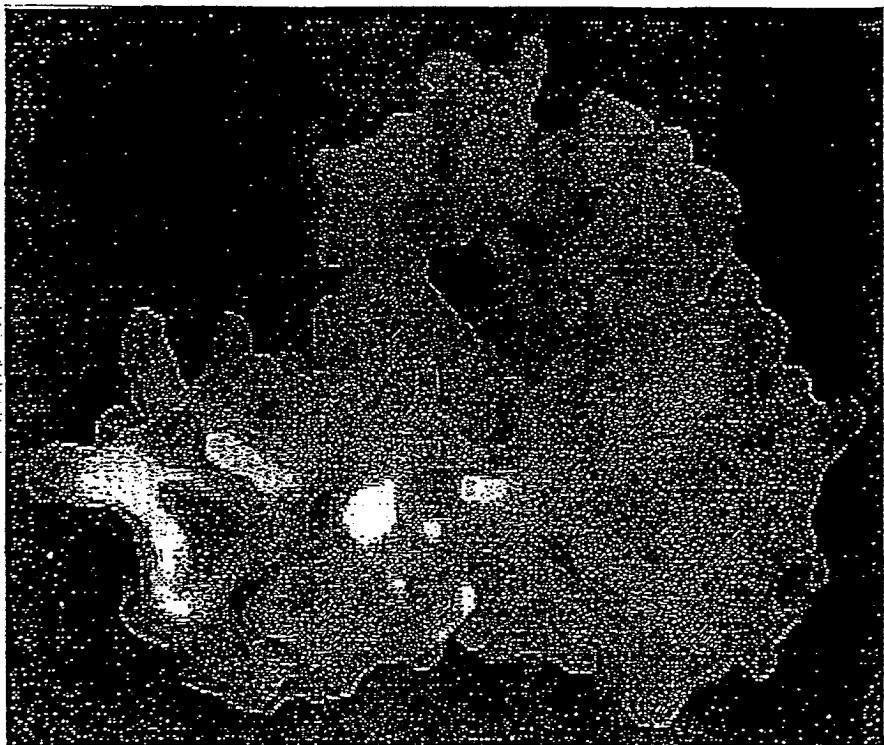


FIGURE 69



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FIGURE 70-A

82/127

FIGURE 70-B

130	KMVENCKYLLSLMGIPYYVEAPSEGEAOASYMAKKGOVVAVVSDYYDALLYGAPRVVRNLTTIKEM-----	MJAFENI PRO					
130	MLIEDAKKLLLEMGMGIPIVOAPSEGEAOAAYMAAKGSVYASASODYSLLFGAPRLVRNLTTGKRKLPGK	PFFUFENI PRO					
136	OHNDECKHLLSLMGIPYLDAPSEAEASCAAALKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIO	HUMFENI PRO					
134	OHNDECKHLLSLMGIPYLDAPSEAEASCAAALKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIO	MUSFENI PRO					
134	EHNEEAQOKLLGLMGIPYLIAPTEAEAOCAELAKKGKVYAAASEDMDTLCYRTPFLLRHLTSEAKKEPIH	YSTS10 PRO					
131	DMIKEVOEELLSRFGIPYTAPMEAEOCAELLOLNVDGIIITDSDVFLFGGTKIYKNMFHHEKNY---VE	YSTRA02 PRO					
131	VMIKECOEELLRLFGLPYIVAPOEAEOCSKLELKLVDGIVTDDSDVFLFGGTRVYRNMFNONKF---VE	SPORAD13 PRO					
131	OMFLESOEELLRLFGIPYIOAPMEAEOCAAILDLTDOTSGITIDOSDIWLFGARHVYRNFFNFKF---VE	HUMXPG PRO					
131	OMFLESOEELLRLFGIPYIOAPMEAEOCAVLDLSDOTSGITIDOSDIWLFGARHVYKNFFNFKF---VE	MUSXPG PRO					
131	OMCLESOELLRLFGIPYIVAPMEAEOCAAILDLTDOTSGITIDOSDIWLFGARHVYKNFFSONKH---VE	XENXPG PRO					
111	DHVYKTNALLTLEGIKVIAPGDEAOCARLEDLGVTSGCITTDFDYFLFGGKNLYRFDTAGT-----	CELRA02 PRO					
150	160	170	180	190	200	210	
195	- - - - - PELIELNEVLEDLRLISLDDLIIDIAIFMGTQYNNPGGV--K---GIGFKRAYELVRSVGAK--DV	MJAFENI PRO					
200	NVYVE- IKPEL ILEEVLKELKL TREKLIELAIIYGTQYNNPGGI - - K -- GIGLKKALEIVRHSKDPLAKF	PFFUFENI PRO					
206	EFHLSRILLOELGLNOEOFVDLCLLGSOYCESIRGICPKRAVDLIOK--HKSIEEVIRRLDPN---KY	HUMFENI PRO					
204	EFHLSRVLROELGLNOEOFVDLCLLGSOYCESIRGICAKRAVDLIOK--HKSIEEVIRRLDPS---KY	MUSFENI PRO					
204	EIDTELVLRGDLTIEOFVDLCLMGLCGOYCESIRGVCPVTALKLIK T--HGSIEEKIVEFIESGESNTKW	YSTS10 PRO					
198	FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKGMGPVSSIEVIAEF--GNLKNFKDWYNNGODDKRK	YSTRA02 PRO					
198	LYLMDMKREFNVNOMDLIKLAHL.LGSDOYTMLGLSRVGPVLALEILHEFPGDGTGLFEFKKWFORLSTGHAS	SPORAD13 PRO					
198	YOOYVDFIHNOLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGRGLDPLLKFSEWWHEAOKNP	HUMXPG PRO					
198	YOOYVDFYSOLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGOOGLEPLVKFKEWWSEAOOK	MUSXPG PRO					
198	YOOYADIHNOLGLDRSKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGRGLDPLLKFSEWWHEAONNK	XENXPG PRO					
175	- - - - - SSTAACLHDIMHLSLGRMFM-----	CELRA02 PRO					
220	230	240	250	260	270	280	

FIGURE 70-C

290	300	310	320	330	340	350
251 LKKEVEYYDEIKRIFKEPKV - - - - -	265 OKOSDVLAYAIKEFFFLNPPV - - - - -	269 PVOPENWLHKEAHLFLEPEV - - - - -	267 PVOPENWLHKEAOOLFLEPEV - - - - -	272 KIPEDWPYKOARMLFLOPEV - - - - -	265 OETENKFEEKDLRKKLVNNE I LDODDFPSVMMVYDAYMRPEVHDHTTPFVWGVSPORAD13 PRO	268 KNOVNTPVKKRINKLVGK - - ILPSEFPNPLVDEAYLHPAVDDSKOSFOQWGIPOLDELROFLMATTGVWSKO
268 KIRPNPHOTKVKKKL - - RTLOLTPGFNPNAVAEAYLKPVVDOSKGSSLWGKPDLOKIREFCORYFGWNRT	268 KVAENPYDTKVKKKL - - RKLOLTPCFPNPAVADAYLRPVGSSRGSSFLWGKPDVDKIREFCORYFGWNRM	268 KMRPNPNDTAKKKKL - - RLLDL00SFPNPAVASAYLKPVVDGESKSAFSWGRDPOLEOIREFCESRFGWWYRL	268 XENXPG PRO	268 CELRAD2 PRO		
194 - - - - EKKVSRPHLISTAILLGGDYFORGVONIGIVSVFD - - ILGEFFGDGNEEIDPHVILDRFAASYVRE						
360	370	380	390	400	410	420
300 RVKKHVDKLYNLIA - - - - -	314 RVKNGLERLKKAI - - - - -	320 RIRSGVKRLSKSROGS - TOGRLDDFFKVVT - - - - -	318 RIRSGVKRLSKSROGS - TOGRLDDFFKVVT - - - - -	323 RVKSGISRLKKGLKSG - IOGRLDGFFFOVV - - - - -	335 KSOEILIPLIRDVNRKK - - - - -	337 RTNEVLLPVIODMHKKOF - - - - -
336 KTDDESLFPVLKOLDAAOTOLRIDSSFFRLAQOEKEDAKRIKSORLNRAVTCMLRKKEKAASCIEAVSVAM	336 KTDDESLYPVLKHLNAHOTOLRIDSSFFRLAQOEKODAKLIKSHRLSRAVTCMLRKEREKAPELTKVTEAM	336 KTDDEVLLPVLKOLNAOOTOLRIDSSFFRLEOHEAG--LKSORLRRAYTCMKRKEROVEAEVEAAVAVM	336 EIPARSEDTORKLRLRRKKYNFPVGFPPNCDAVHNATMYLRRPPVSSEIPKIPR - - AANFOOVAEIM	336 CELRAD2 PRO		
84/127						

卷之三

FIGURE 70-D

14	430	440	450	460	470	480	490
15	KRINEFF						
159	SNLTOFFEGGNTVYAPRVAYHFKSKRLENALSSFKNOISNOSPMSEEIQADADAFGESKGSDELOSRIL						
106	EKEFELLDKAKRKTKRGITNTLEESSSSLKRKRLSDOSKRKNNTCGGFLGETCLSESSSGSSEHAESSSLM						
106	EKEFELLDOAKGKTOKREL PYK						
103	ERECTNORKGOKTNKS						
122	MKECGWPATRTOKELALSIRRKVHLTTTVAQTRIPOFFAAATKSKNFTPIVEPCESLEDYISANN						
14	500	510	520	530	540	550	560
14	NKTKOKTL						
27	KSGKOSTL						
152	KKKAKTGAAG						
50	KKKAKTGGAG						
154	NKKLNKNK						
64	PREYISGOKKLNTSKRISTATGKL						
29	RRKKMASKNSSSDSDSEONFLASLTPTKTNSSSIENPRTKLSTSL						
76	NVORRTAAKEPKTSASDSONSVKEAPVKNGATTSSSSDGGKEKMVLVTARSVFGKKRRLRRARG						
69	SARORSAESESSKIGCSDVPOLVRDSPPHGROGCCVSTSSEDDGEOKAKTVLVTARPVFGKKRRLKLSMK						
58	GSSSDAEDLPSGLIDKOSOSGIVGROKASNKVESSSSDDEDRTVMVTAKPVFOGKKTKSKTMIKE						
187	WYRKRKRSSESPOILLOHHAKROVORK						
	85/127						

FIGURE 70-E

322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTGRR
390 -- RKM
183 SKRRRK
;46 RKRTZ
;38 RRKKT
;23 TVKRK
129 ELGDSD

86/127

MJAFEN I PRO
PFUFEN I PRO
HUMFEN I PRO
MUSFEN I PRO
YST510 PRO
YSTRAD2 PRO
SPORAD13 PRO
HUMXPG PRO
MUSXPG PRO
XENXPG PRO
CELRAD2 PRO

FIGURE 71

S - 3 3

cleavage
site

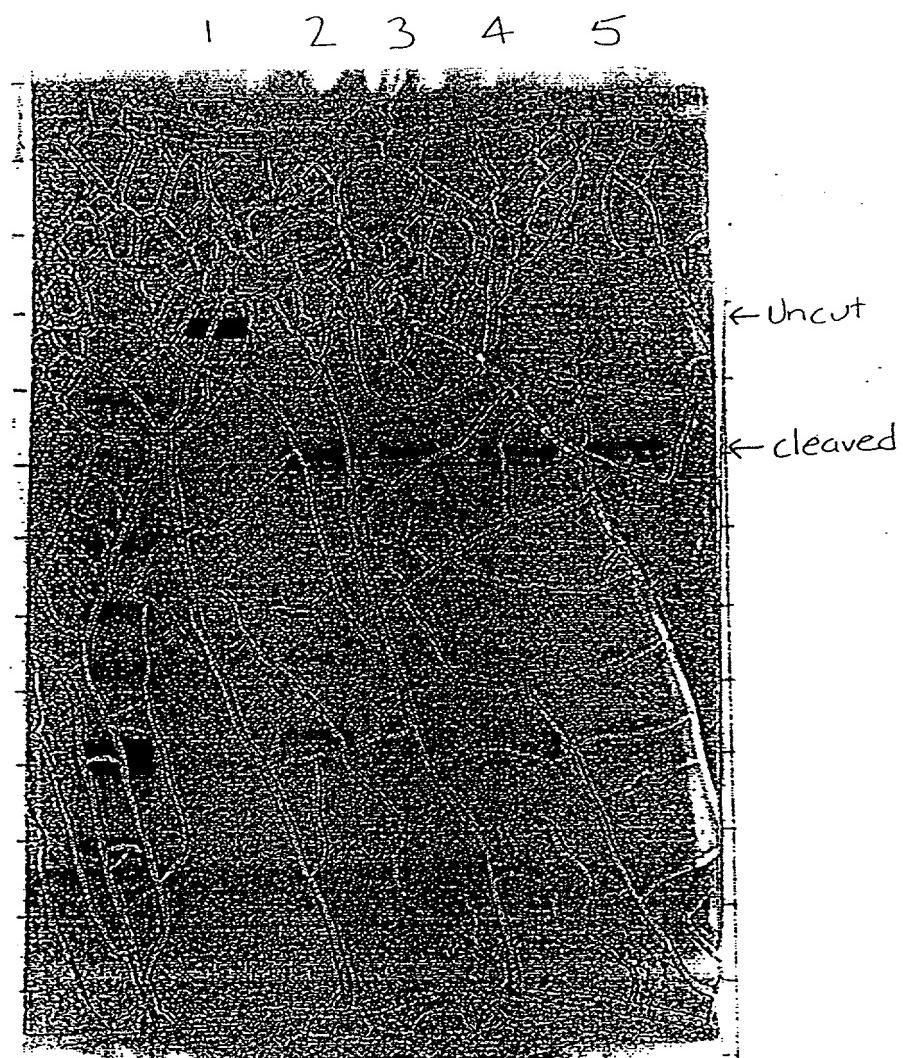
5' T G G Y T C G C T G T C T C G C T G A
T G C G A C A G A G C G A A
3' G

1 1 - 8 - 0

cleavage
site

5' T G C T C T C T C T G G Y T C G C T G T C T G A
G C G A C A G A A A
3'

FIGURE 72



88/127

FIGURE 73

1 2 3 4 5 6 7 8

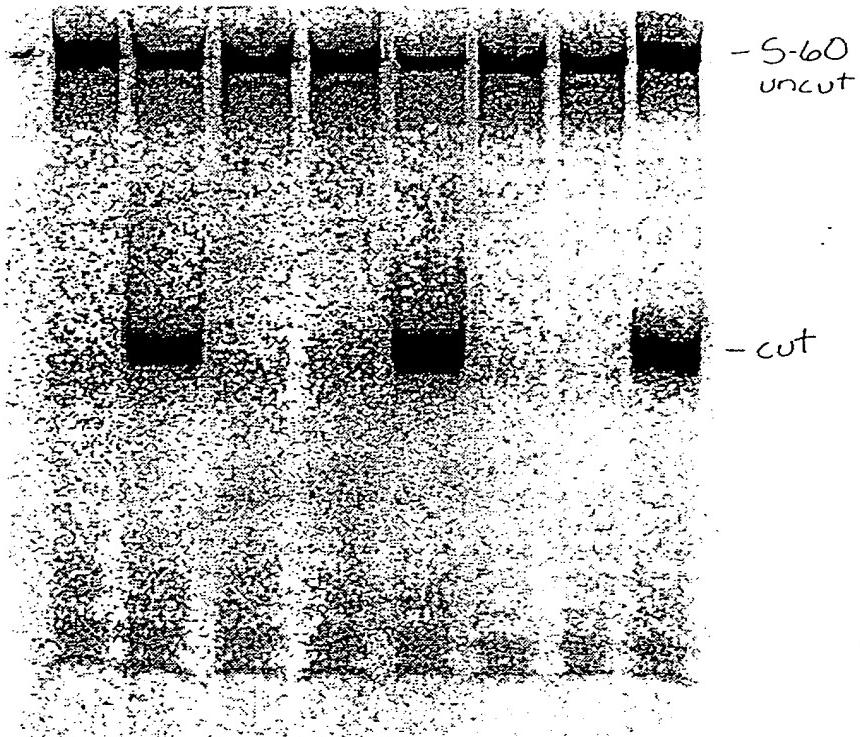
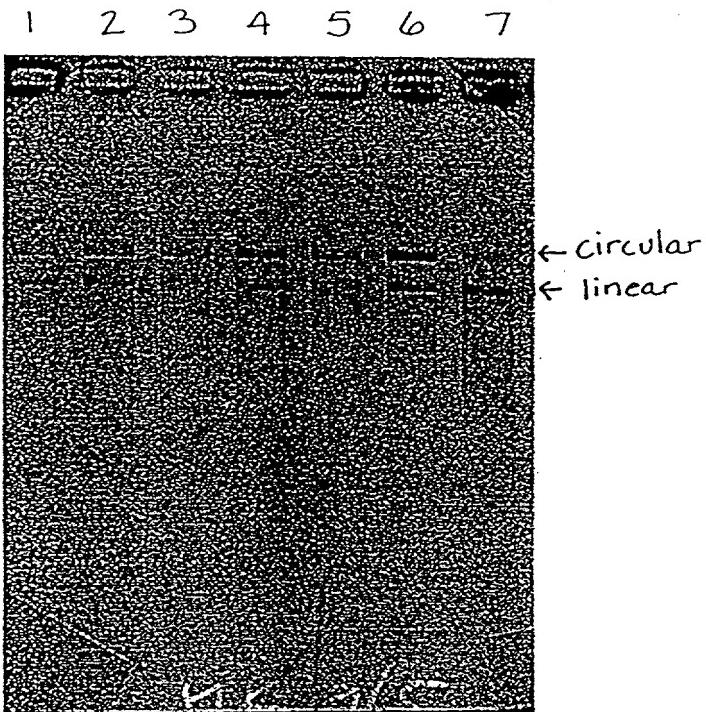


FIGURE 73

89/127

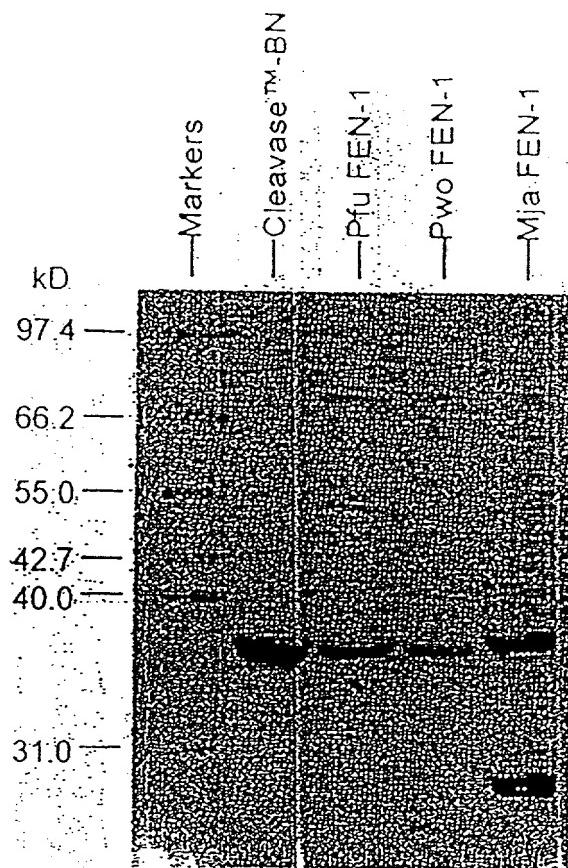


FIGURE 74



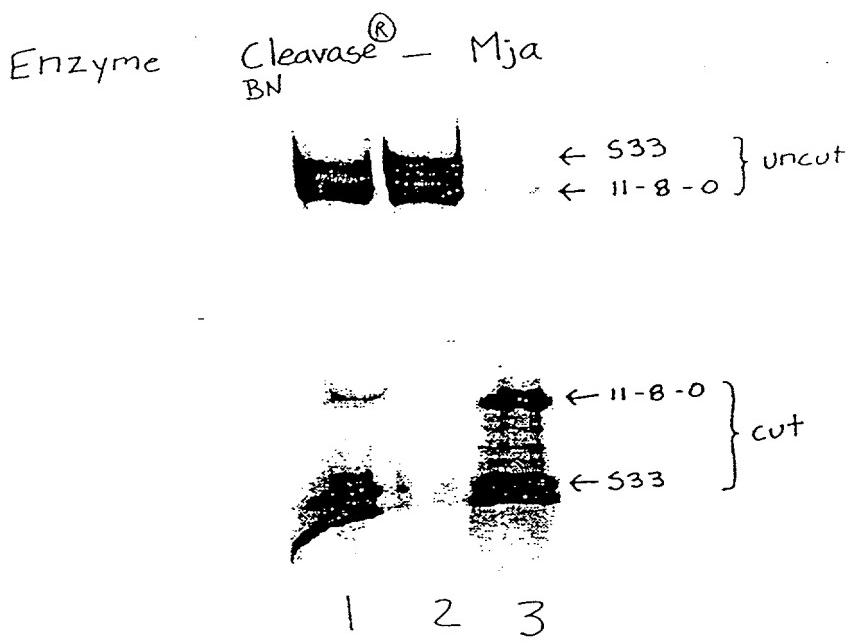
90/127

FIGURE 75

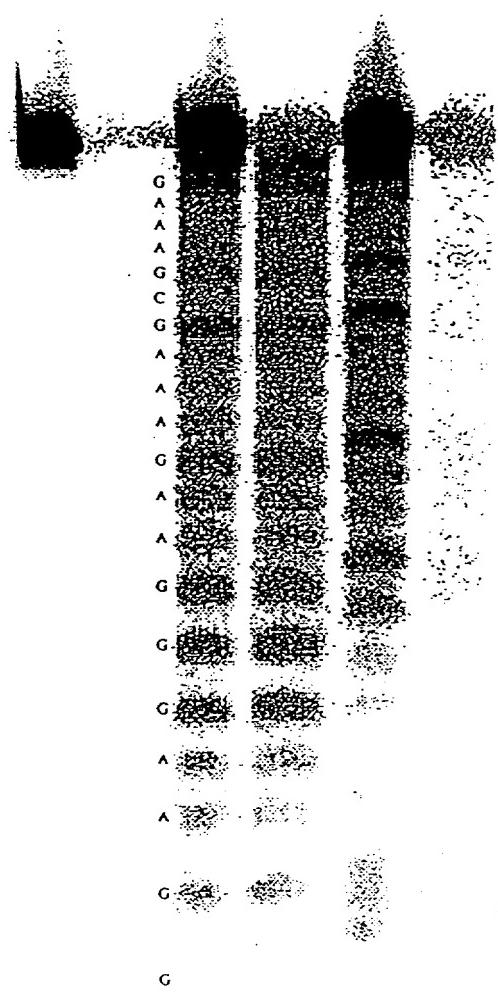
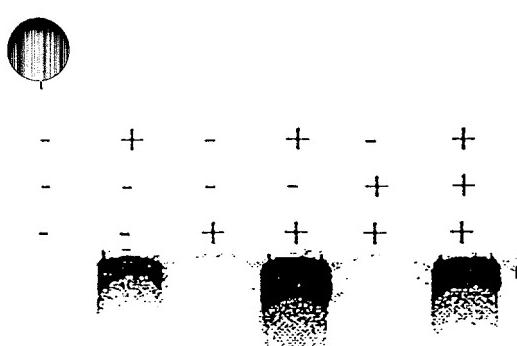


91/127

FIGURE 76



92/127

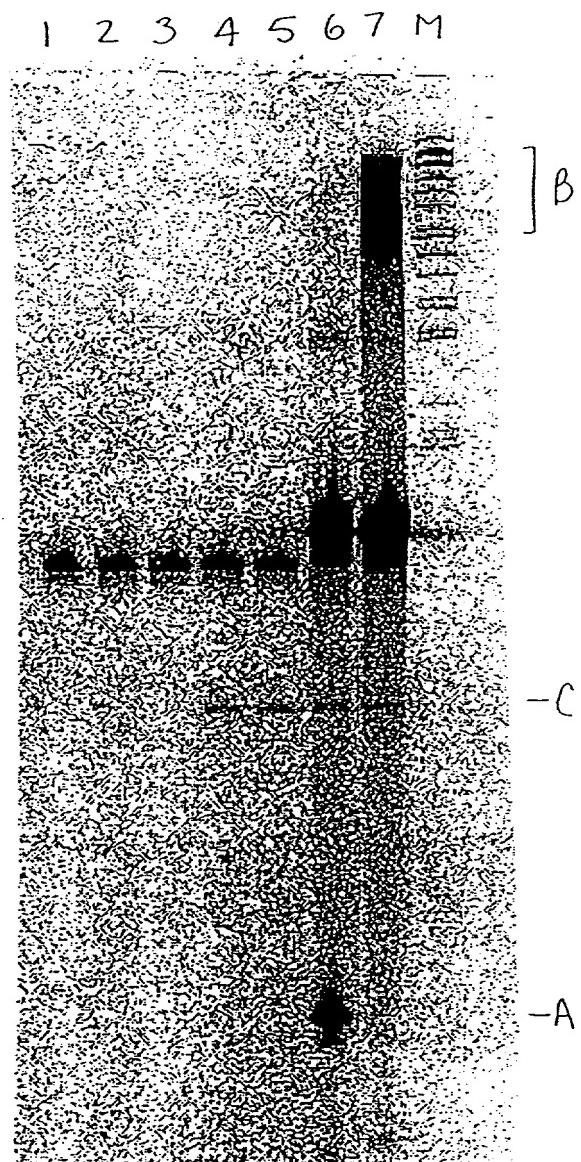


G

5'-nAGAAAGgaagggaagaaagcgaaagG-3'

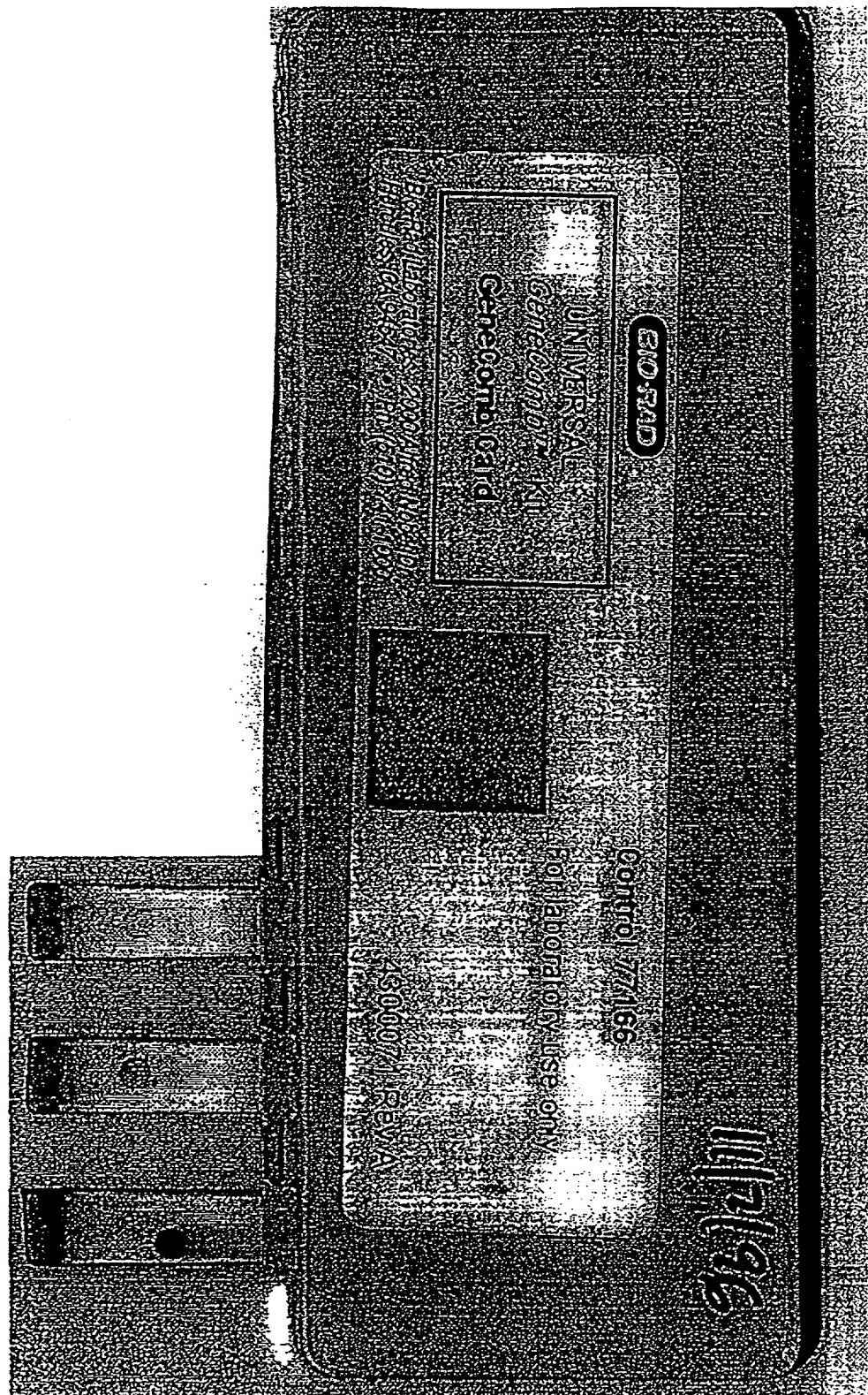
93/127

FIGURE 78



94/127

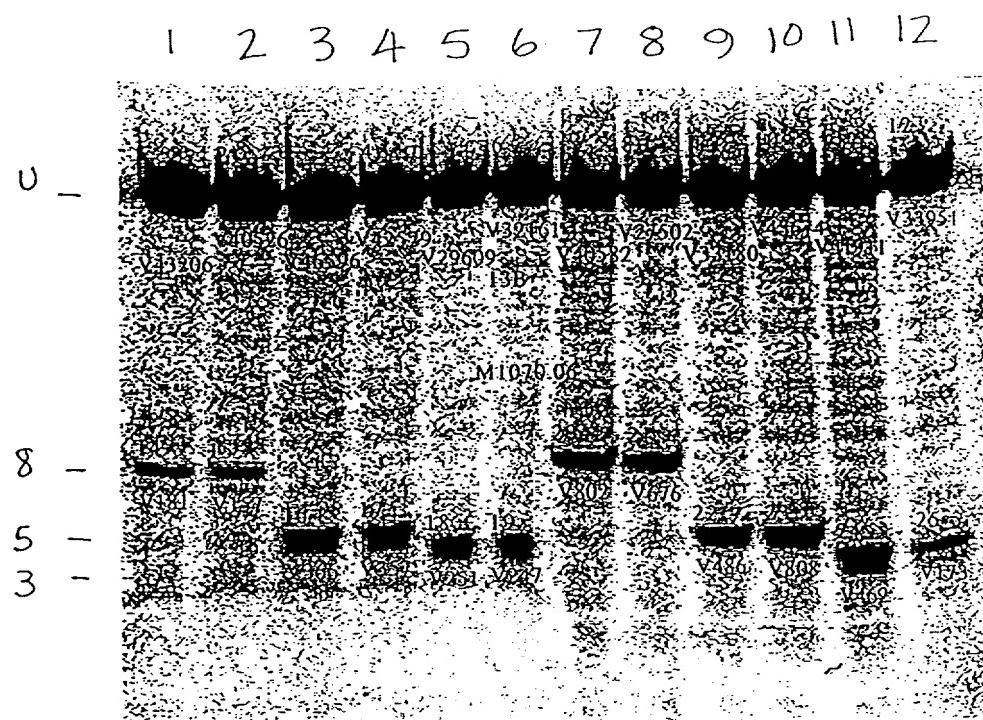
FIGURE 79



6
7
8

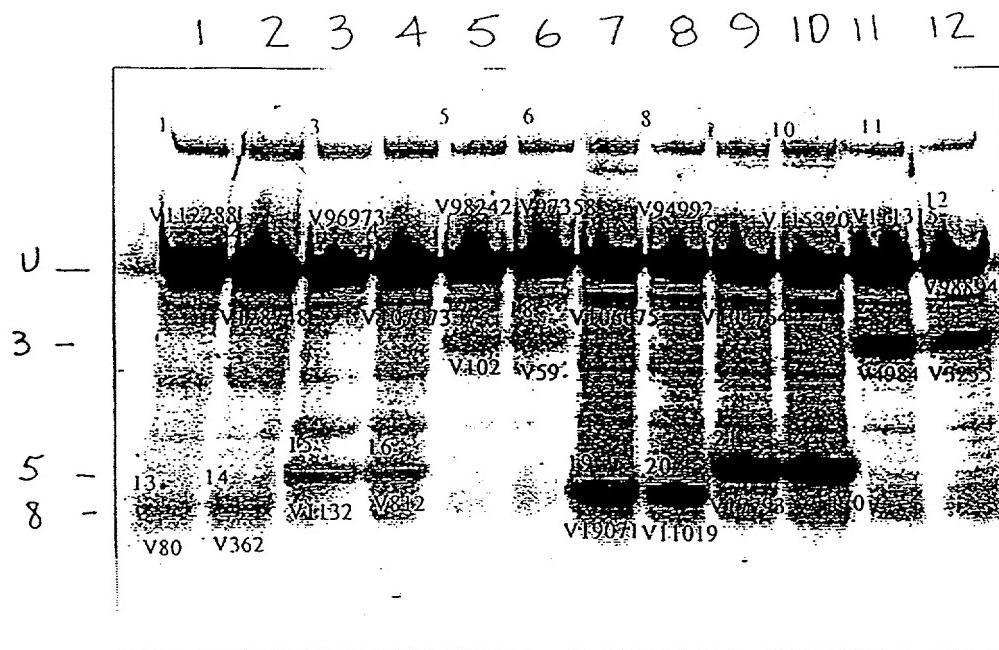
95/127

FIGURE 80



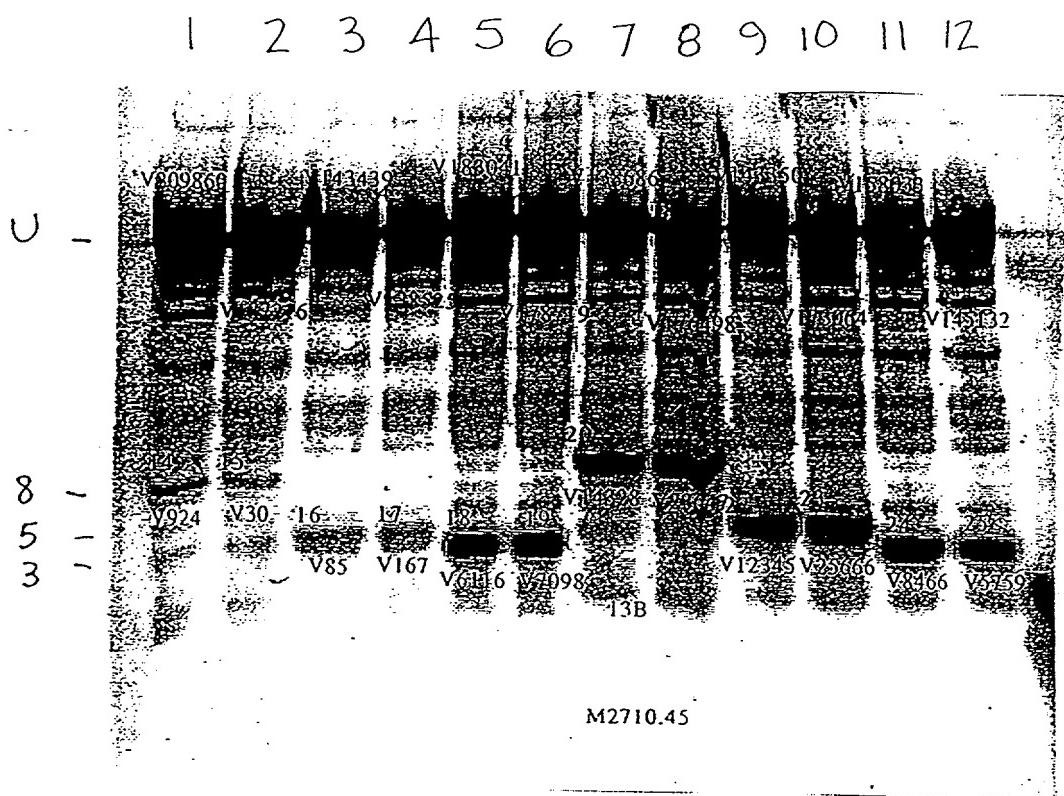
96/127

FIGURE 81



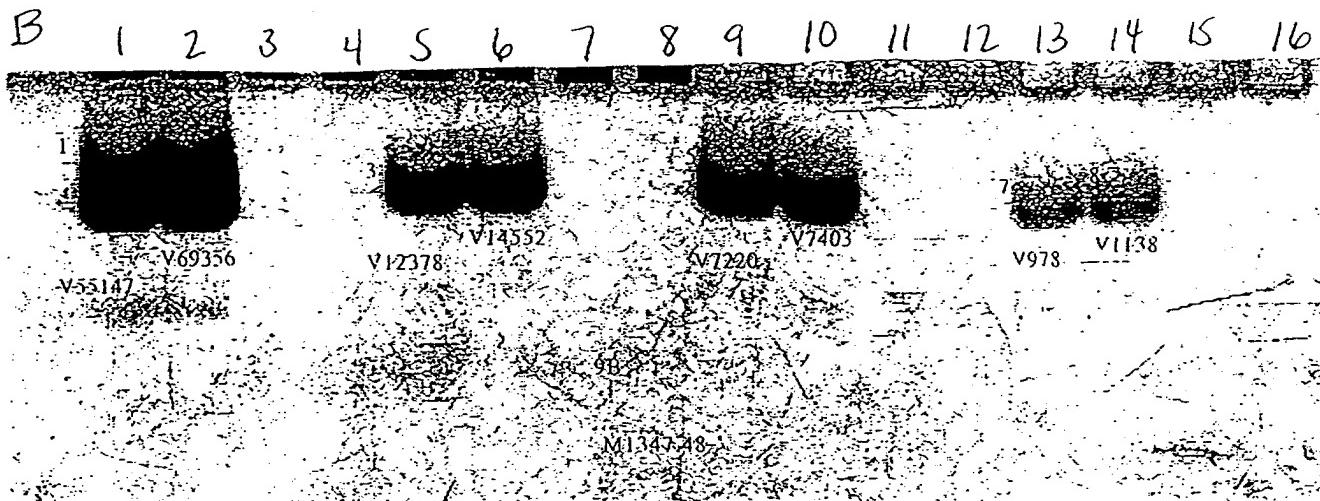
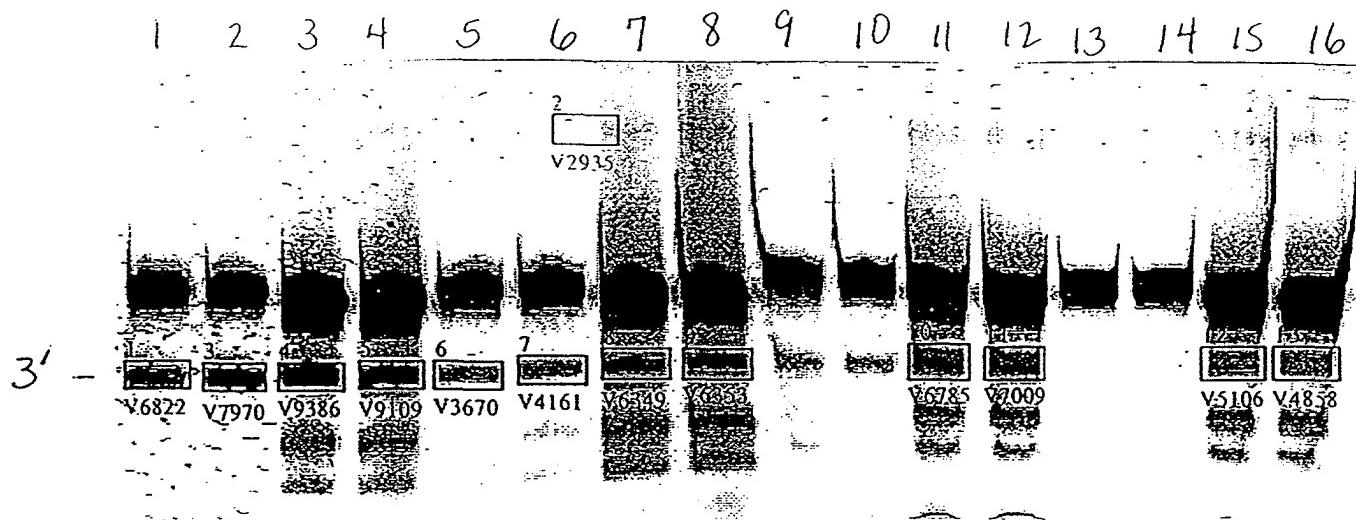
97/127

FIGURE 82



98/127

A



99/127

FIGURE 84

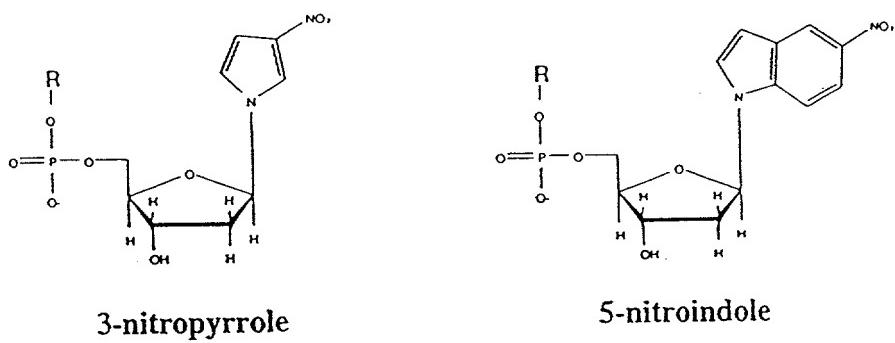
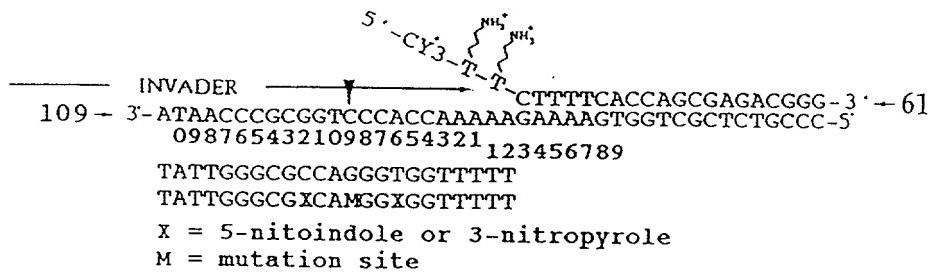


FIGURE 85



101/127

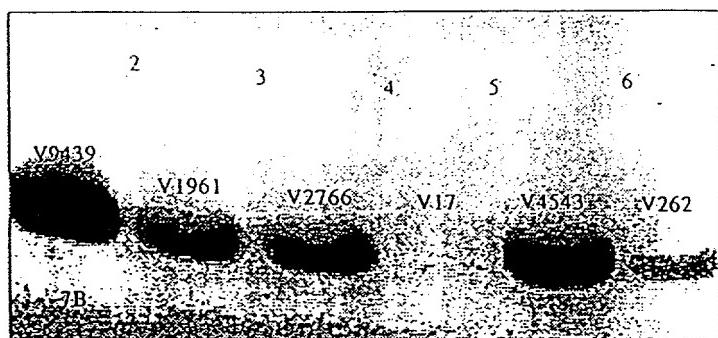
FIGURE 8B

	Base Mismatch	Allcomp 2 NI		Base Mismatch	Allcomp 1 NP		Base Mismatch
NP				1 NP			1 NP

Initial # 67 114 115 116 112 113

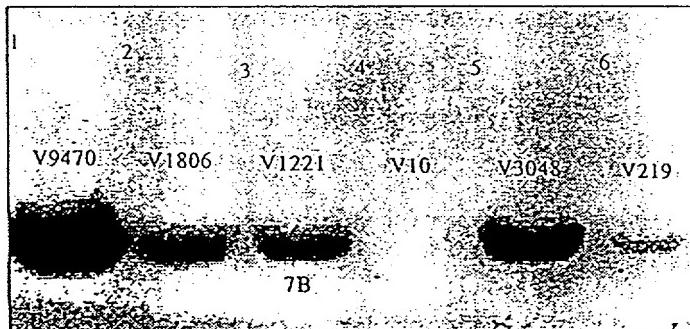
A

52°C



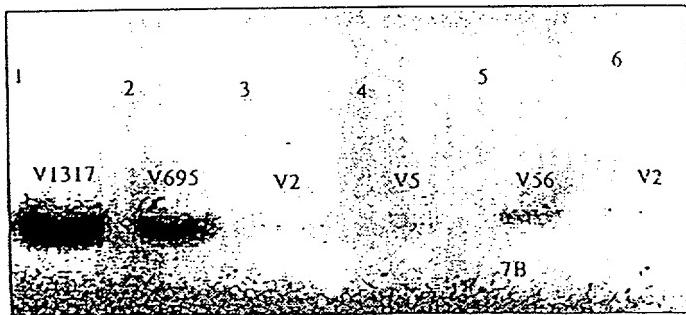
B

55°C



C

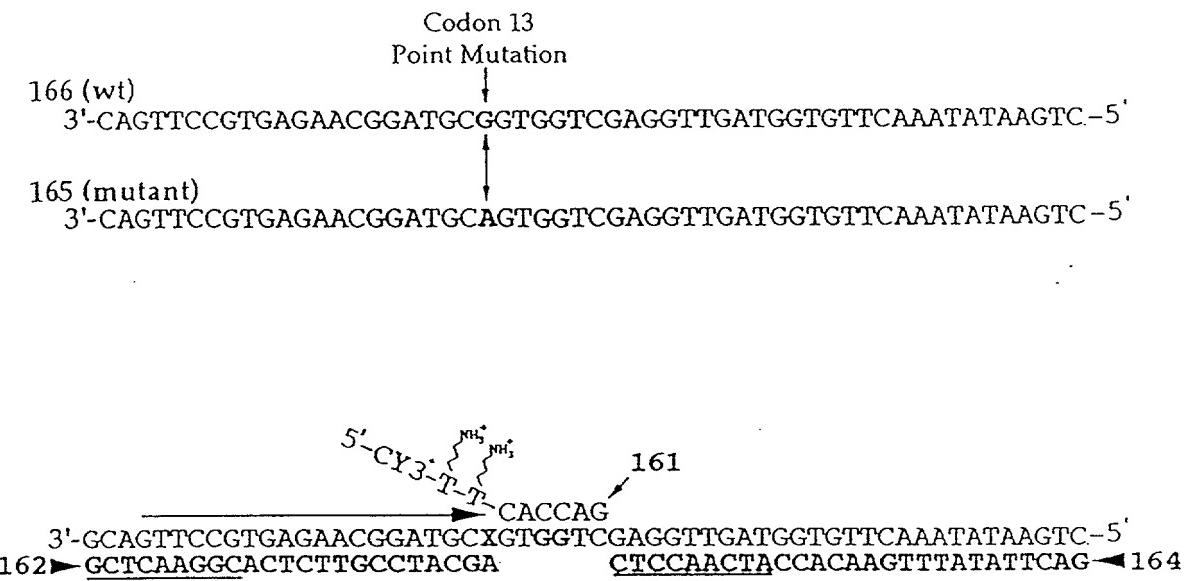
58°C



102/127



FIGURE 87



103/127

FIGURE 88

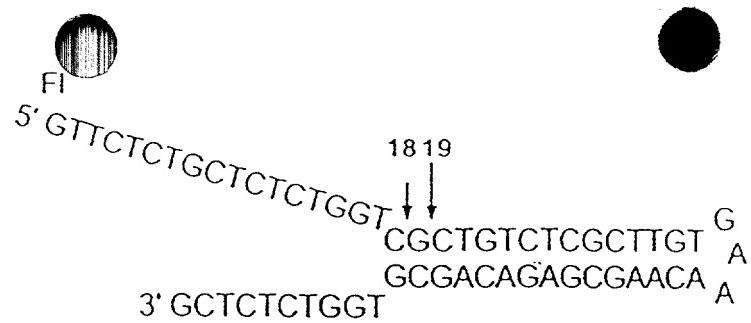
Temp → 47° 50° 53° 56°
Target → — 165 166 165 166 165 166 165 166



104/127

FIGURE 8

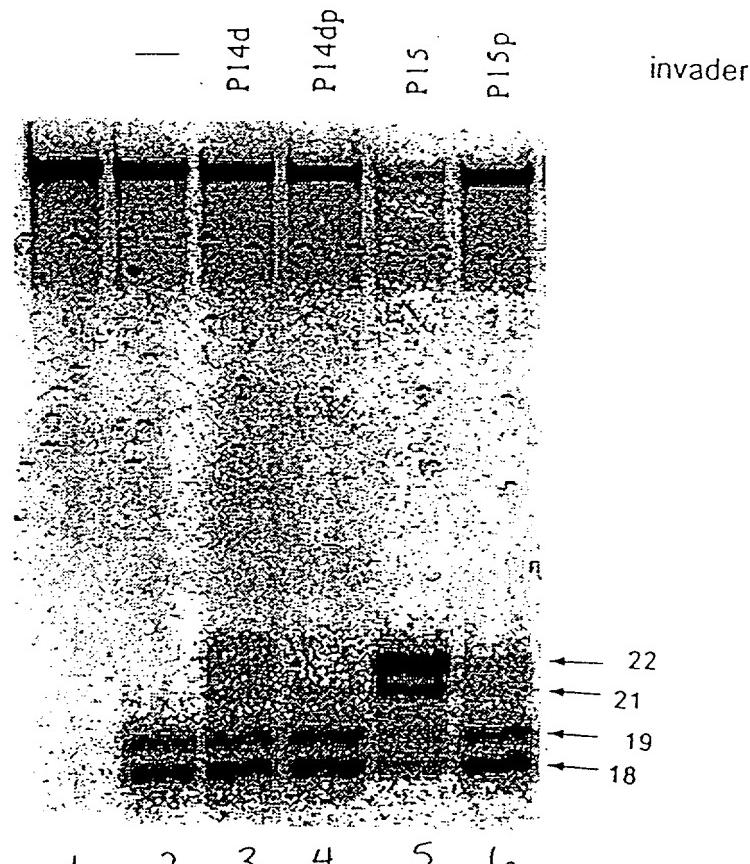
A



B



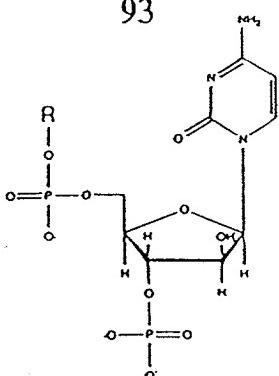
C



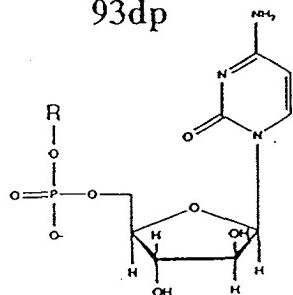
105/127

FIGURE 90
Nucleoside 3'-end Substituents

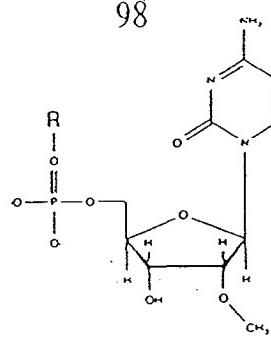
93



93dp



98

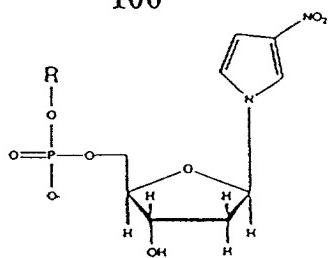


3'-Cytosine Arabinose

3'Phosphate C Arabinose

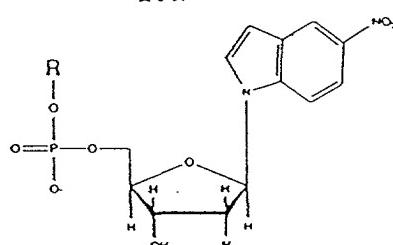
2'-Omethyl Cytosine

100



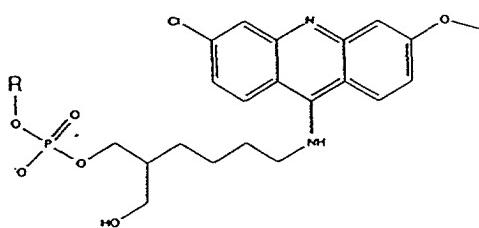
3-nitropyrrole

101



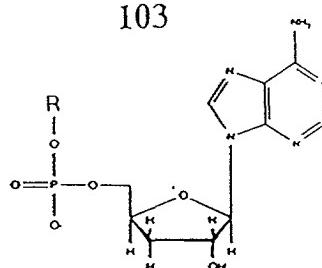
5-nitroindole

102



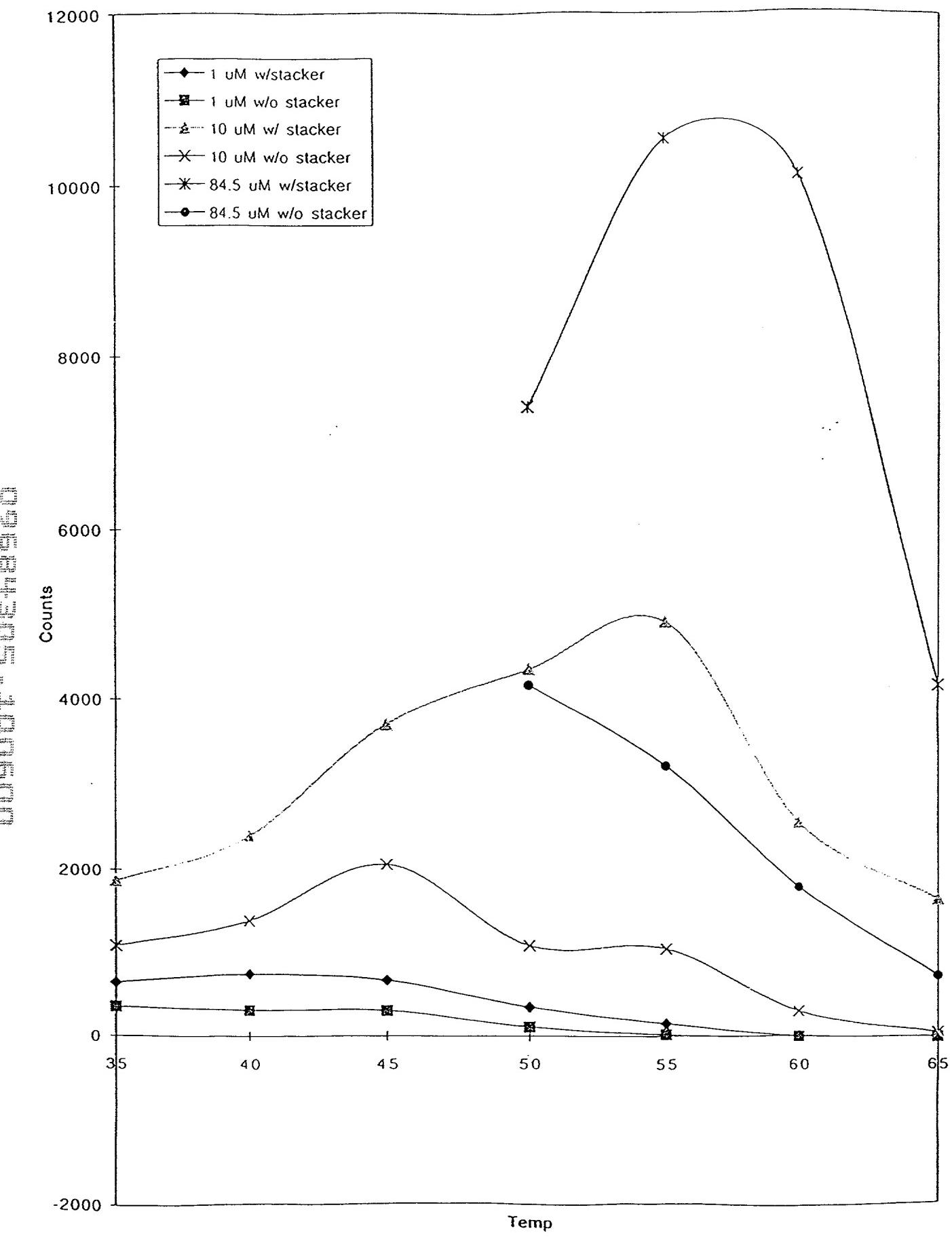
Acridine

103



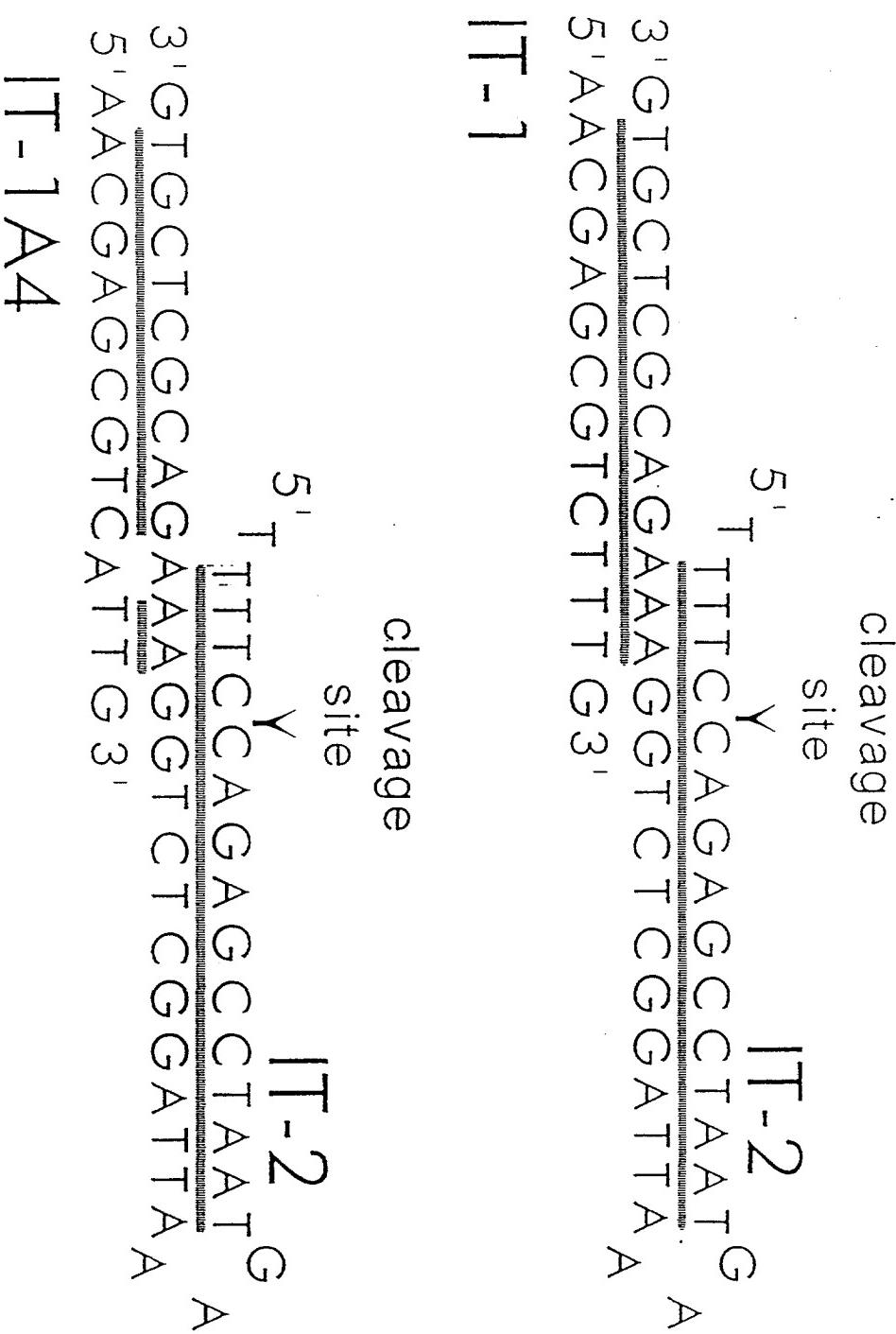
3'-deoxy-adenine

Comparison of Probe w/ and w/o Stacker Temp



167 / 127

FIGURE 92



108/127

FIGURE 93

1 2 3 4



109/127

FIGURE 94

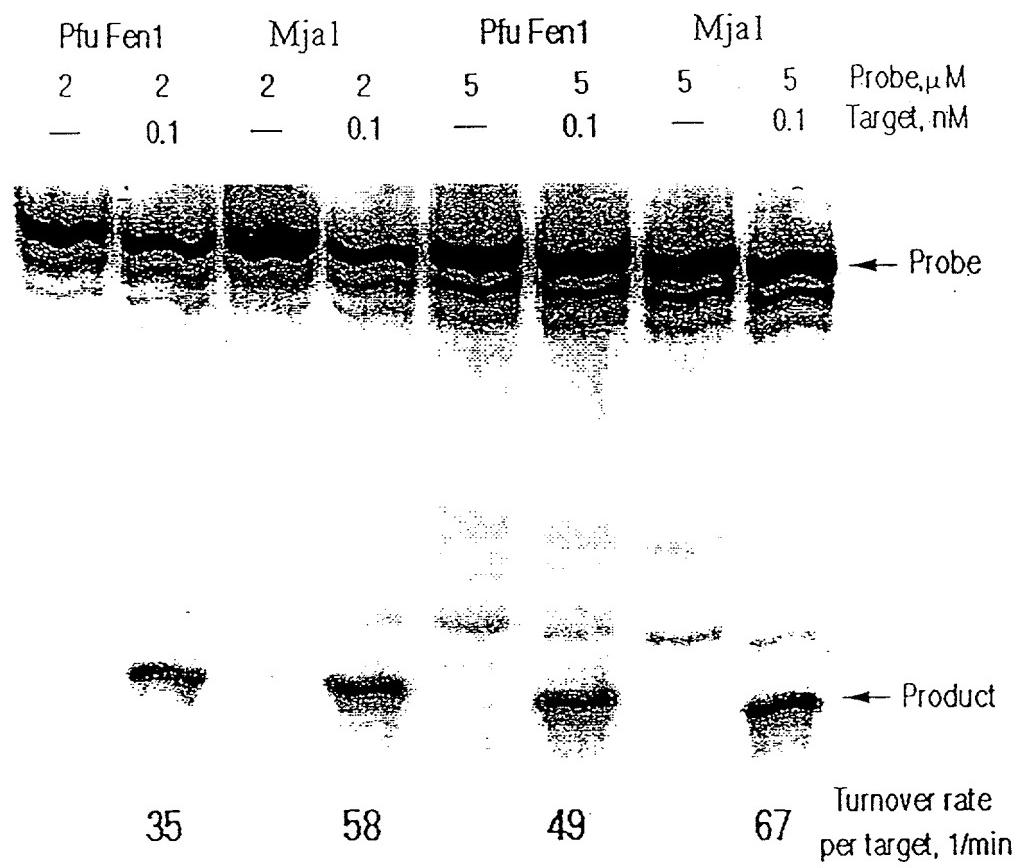
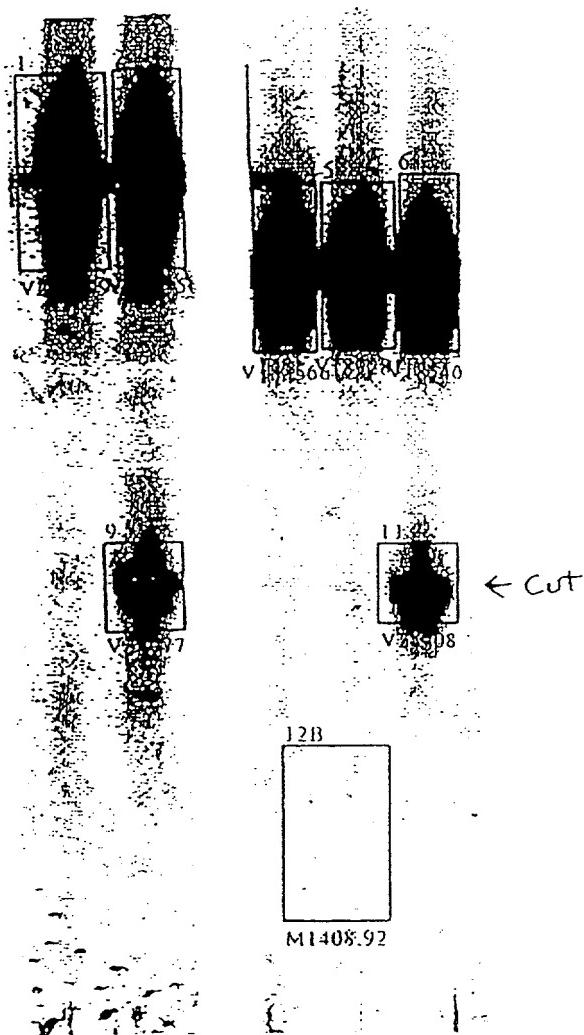


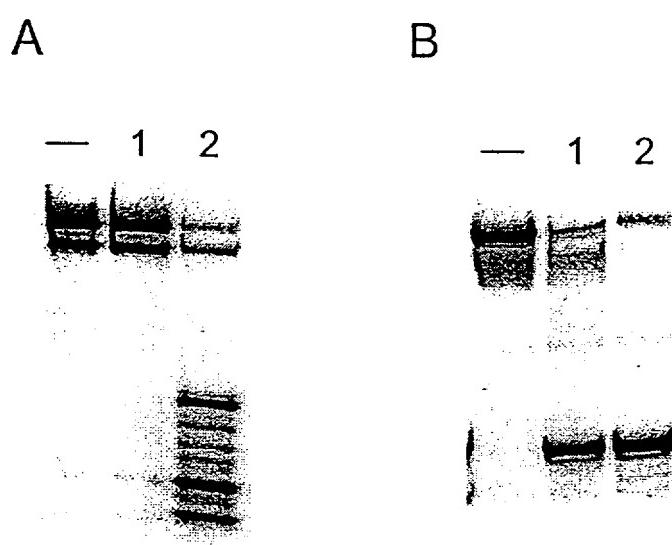
FIGURE 95

1 2 3 4 5



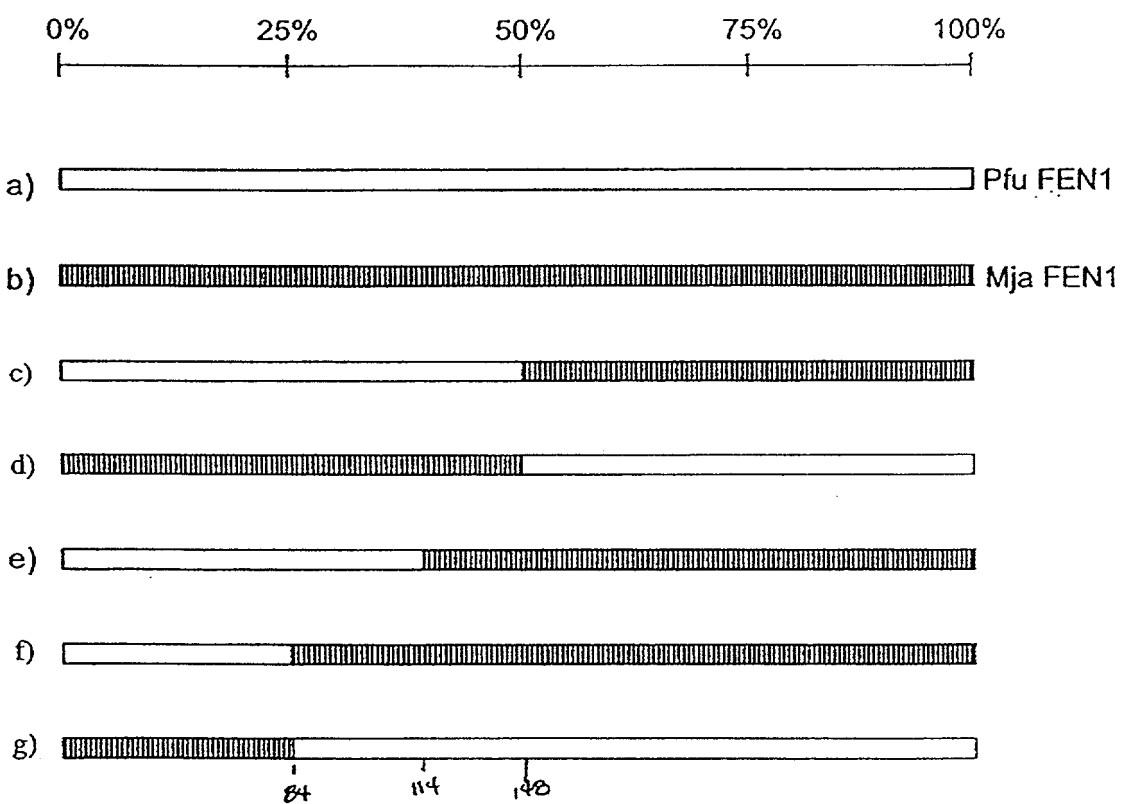
111 / 127

FIGURE 96



112/127

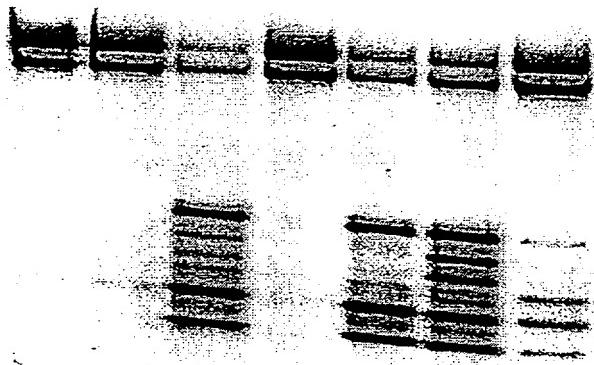
FIGURE 97



113/127

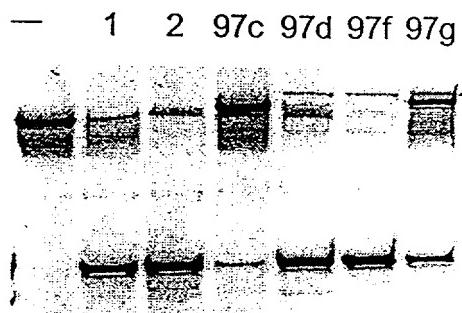
FIGURE 98A

— 1 2 97c 97d 97f 97g



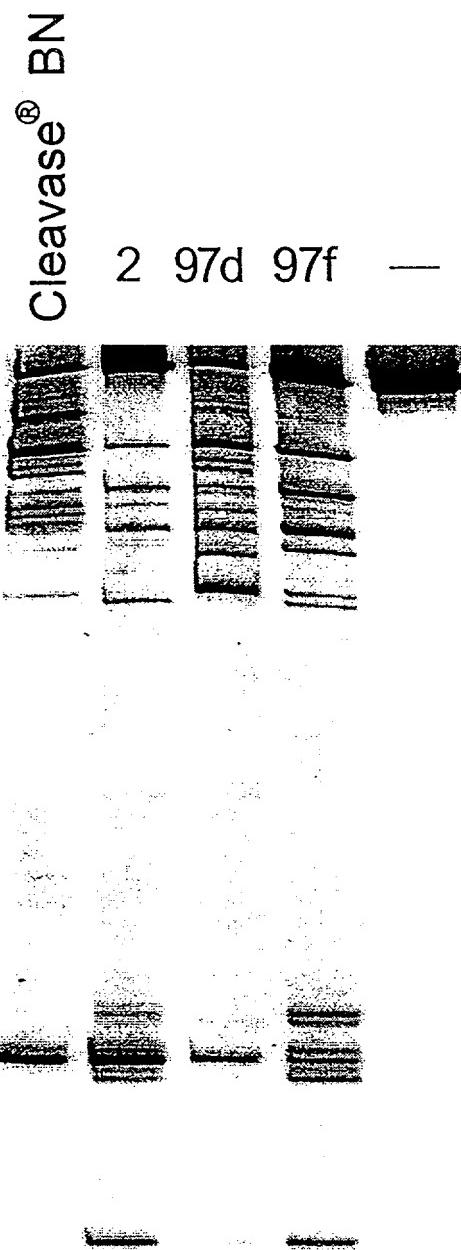
114/127

FIGURE 98B



115/127

FIGURE 99



116 / 127

FIGURE 100

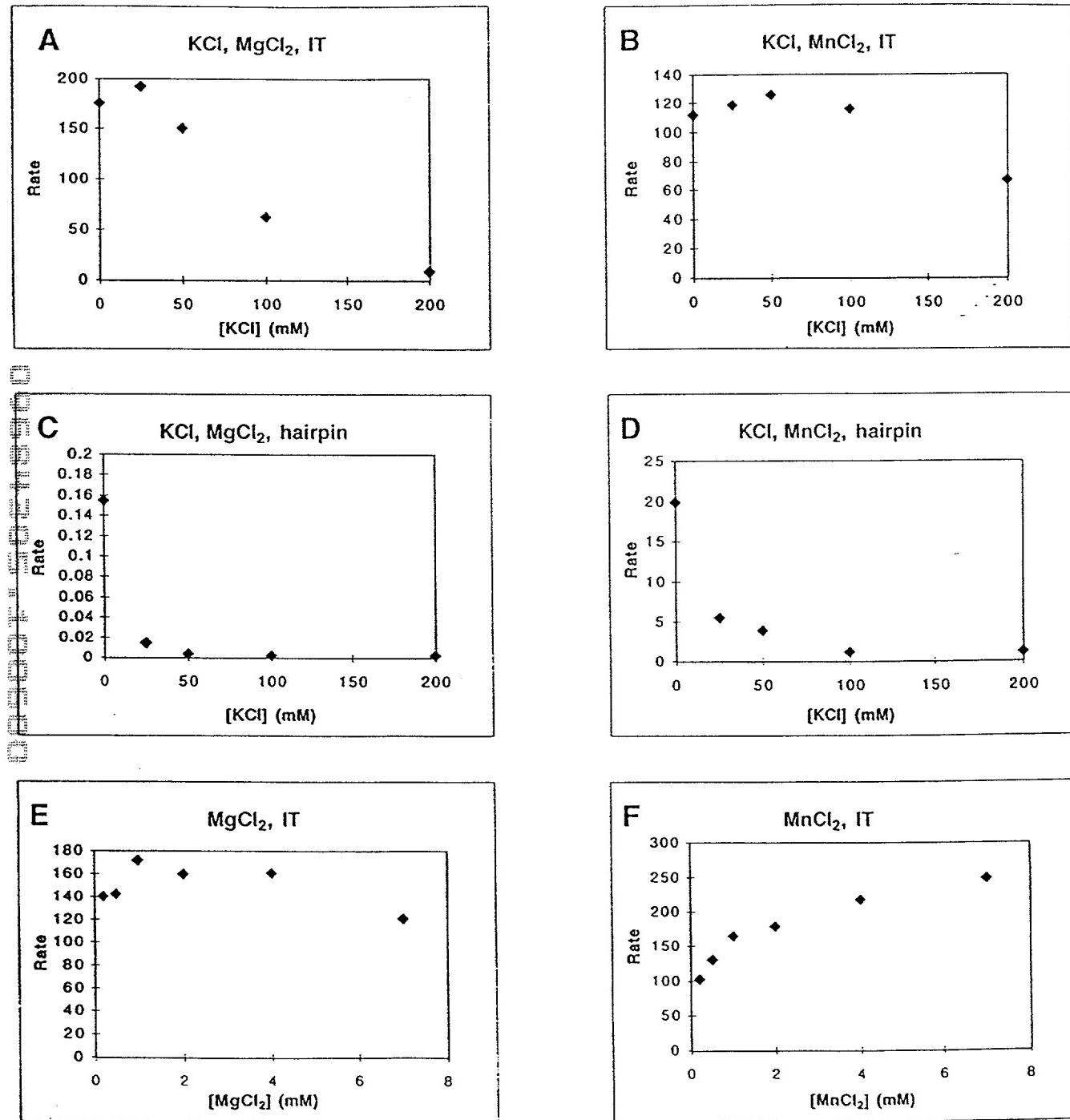


FIGURE 100 (cont.)

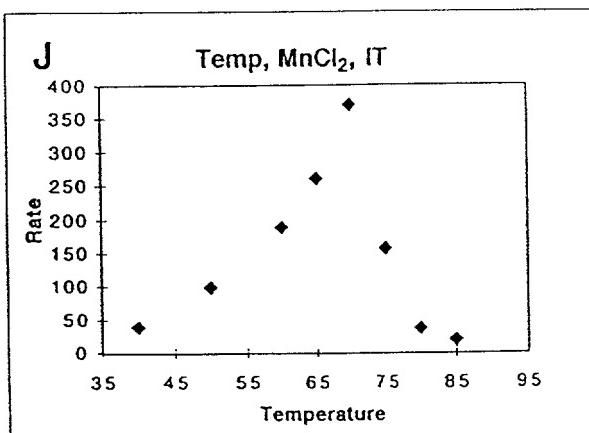
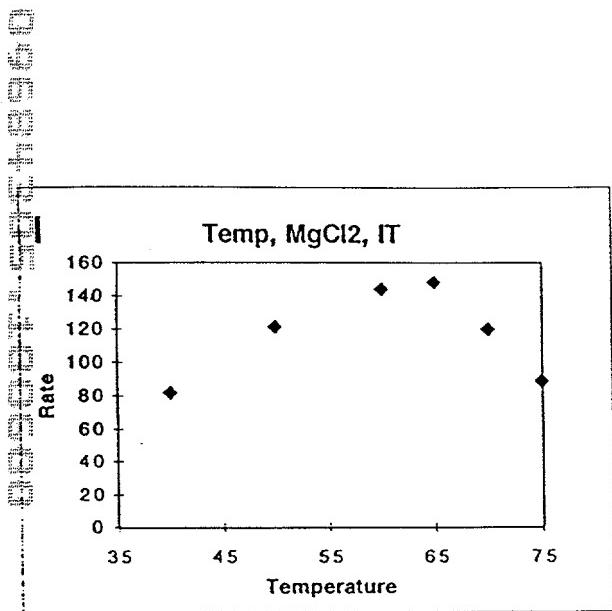
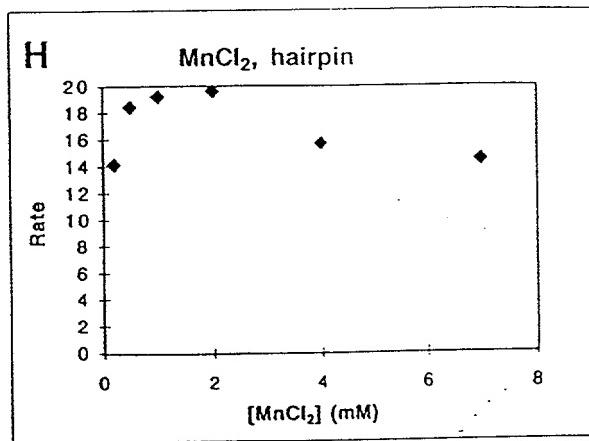
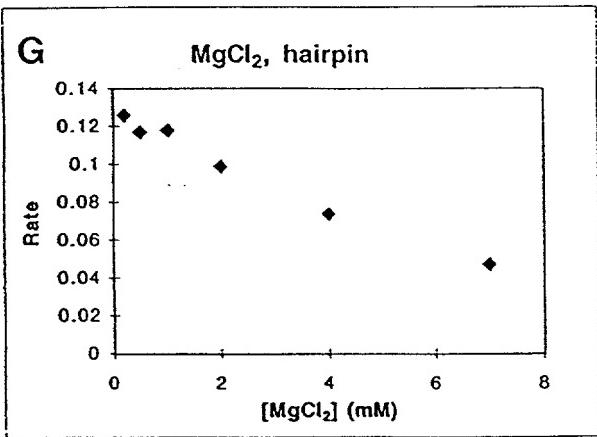
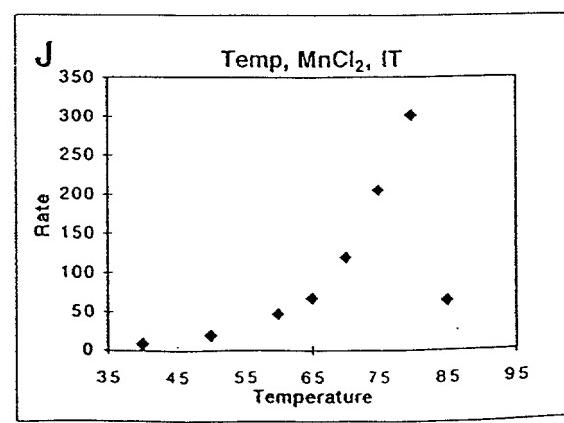
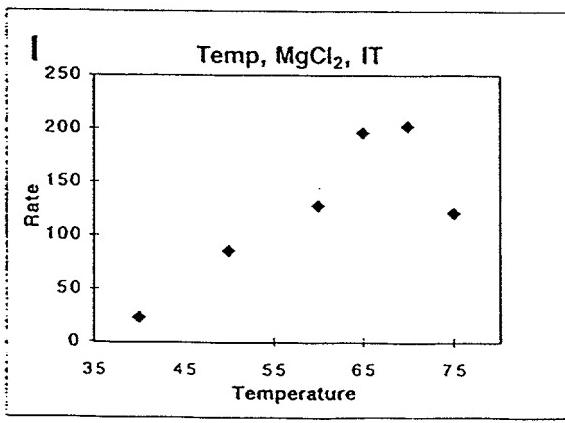
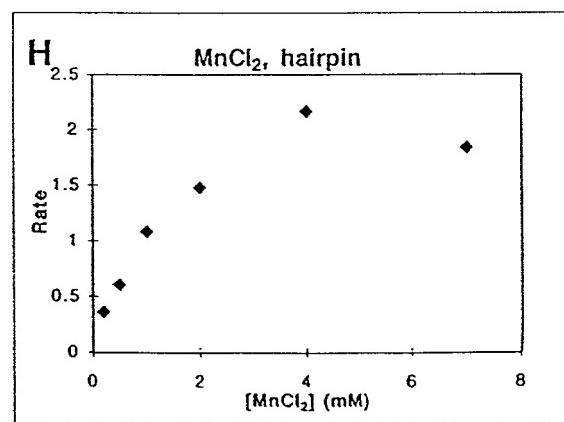
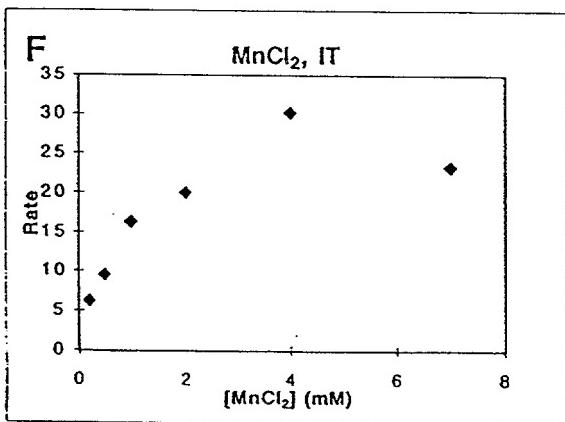
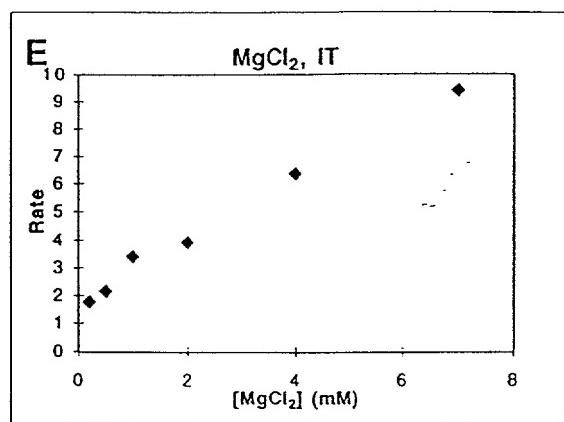
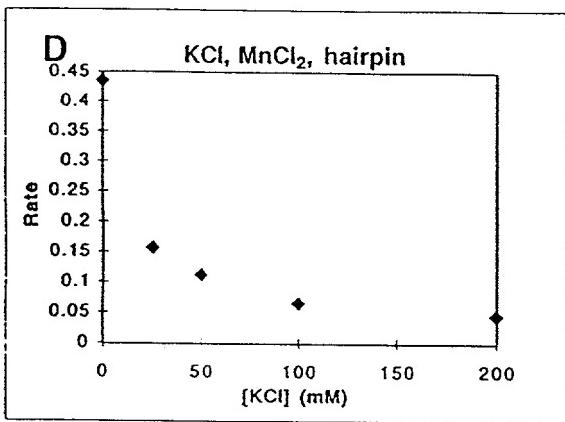
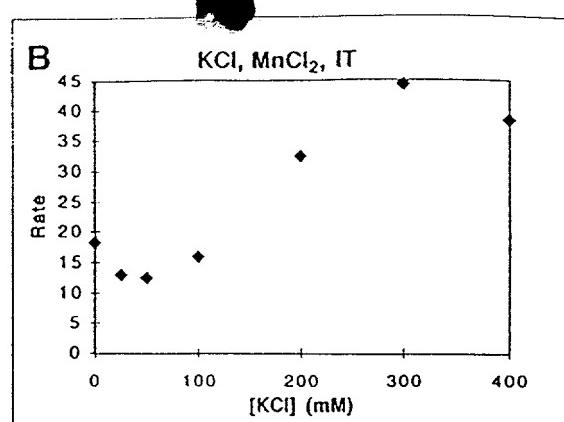
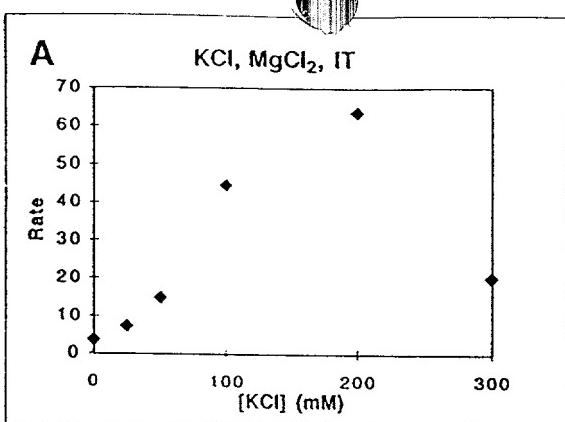
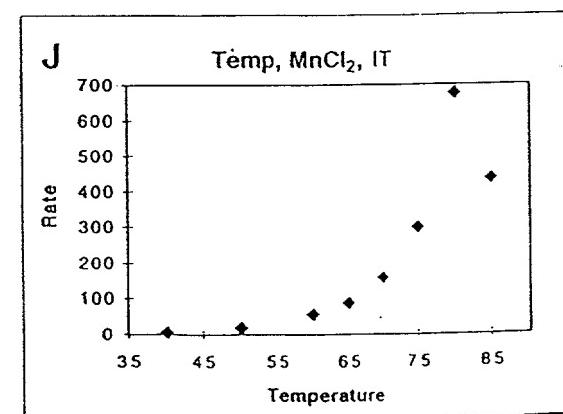
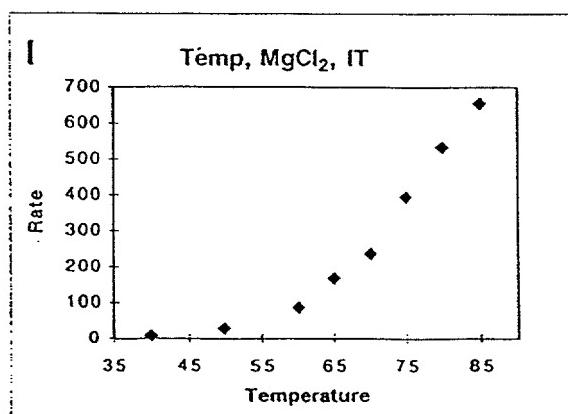
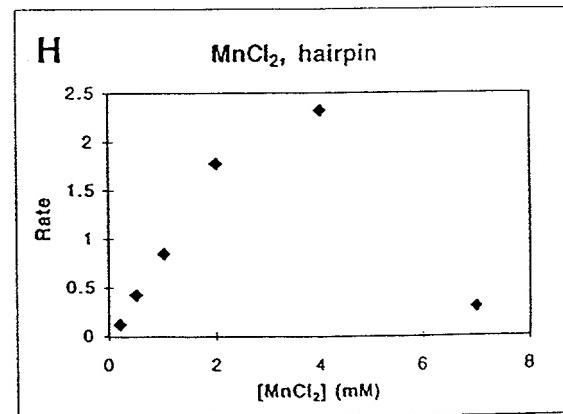
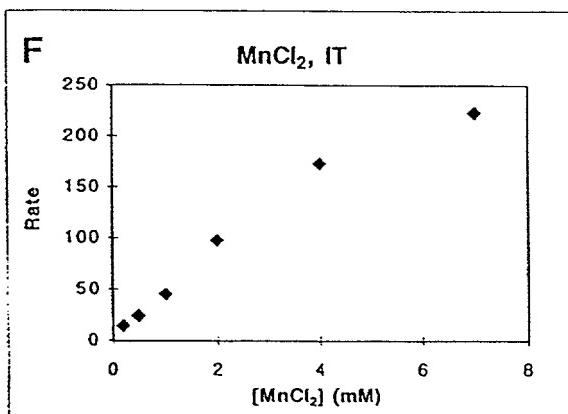
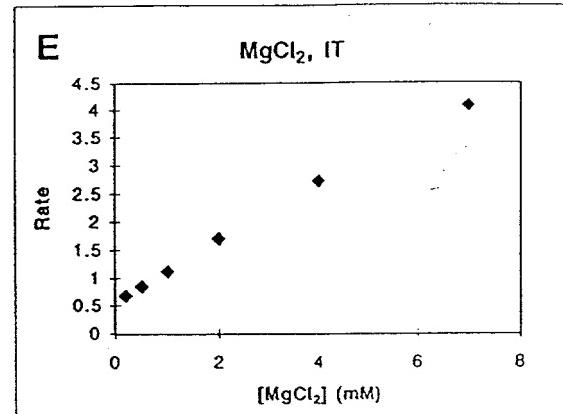
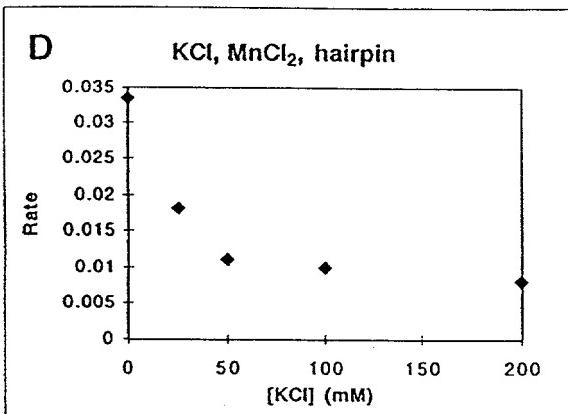
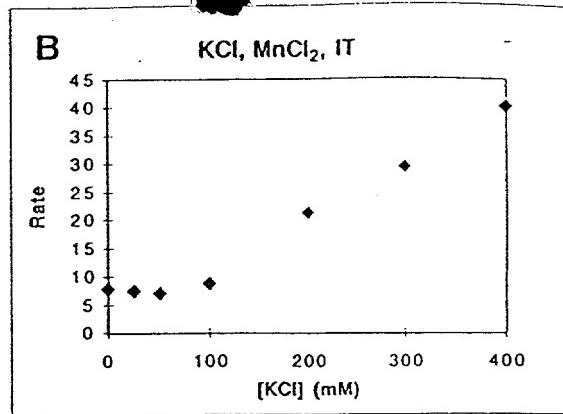
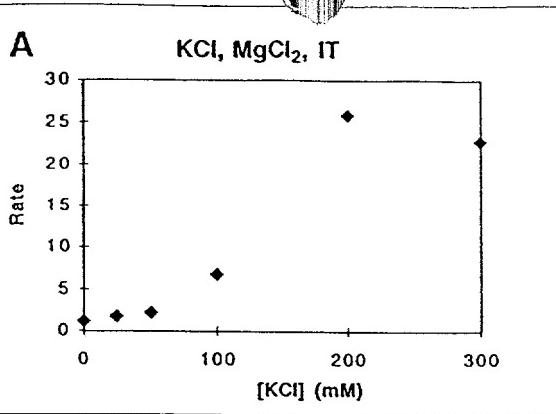


FIGURE 101



119/127

FIGURE 102



120/127

FIGURE 103

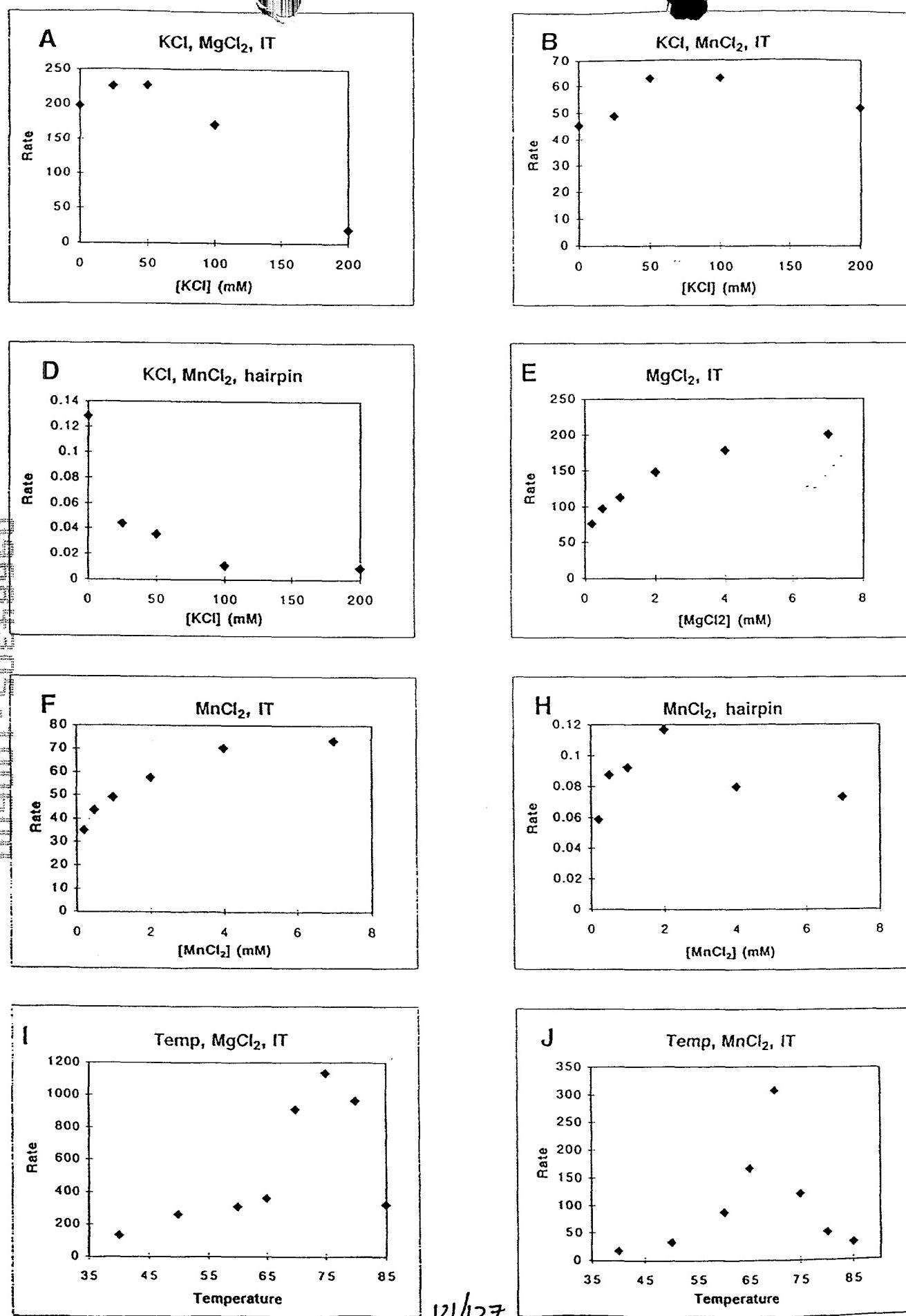
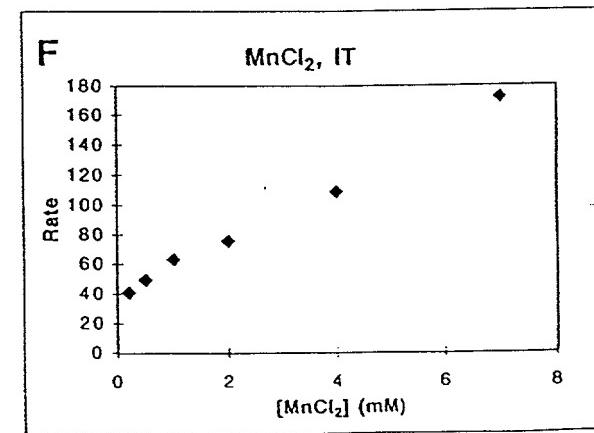
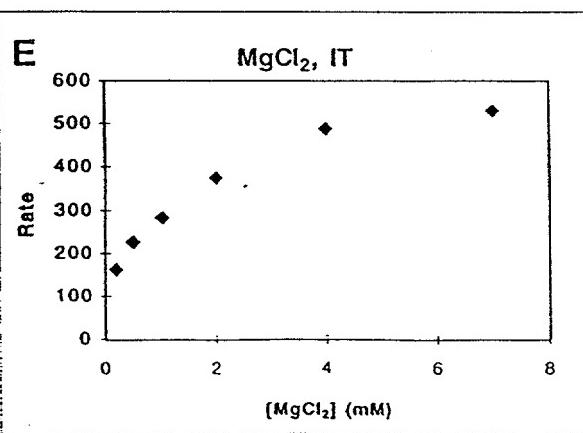
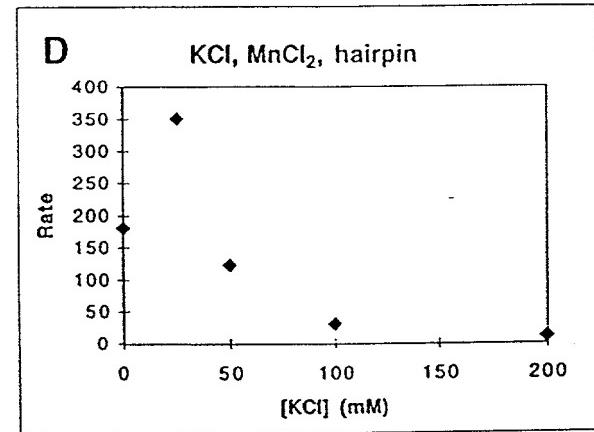
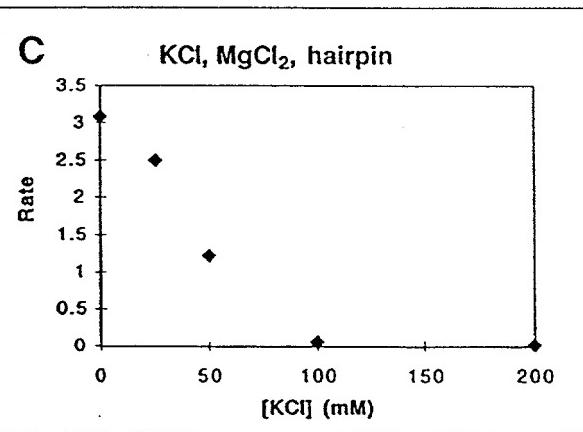
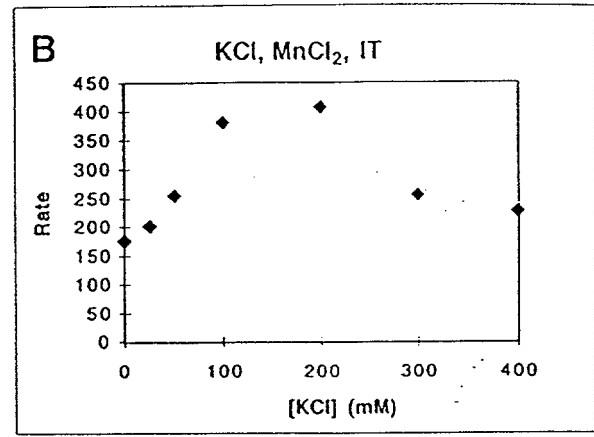
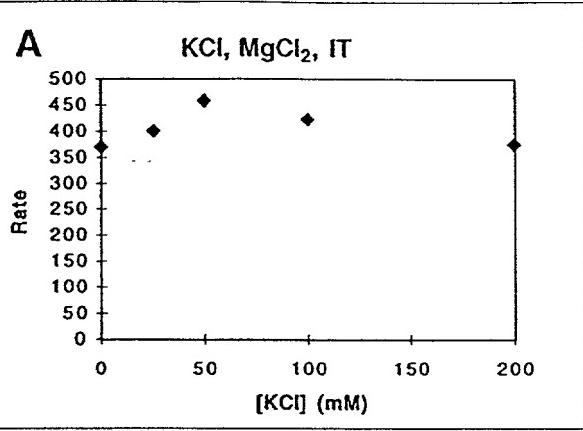


FIGURE 104



122/127

FIGURE 104 (cont.)

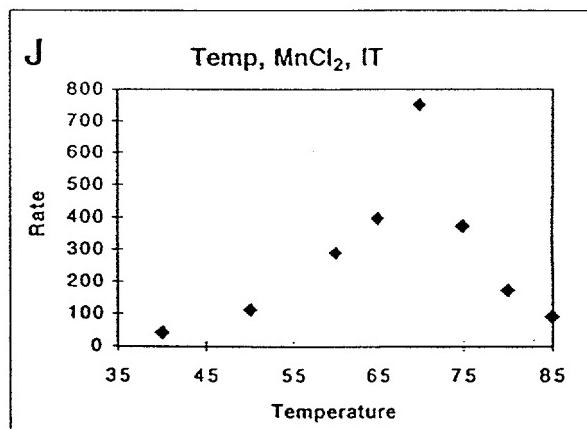
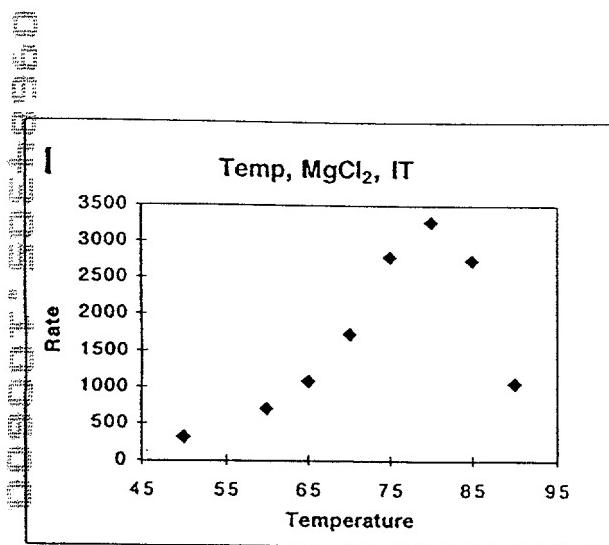
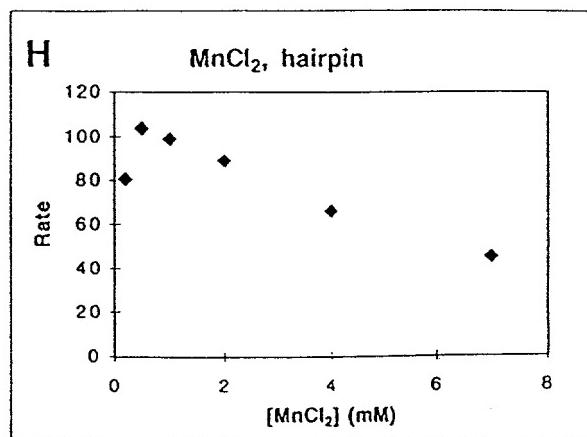
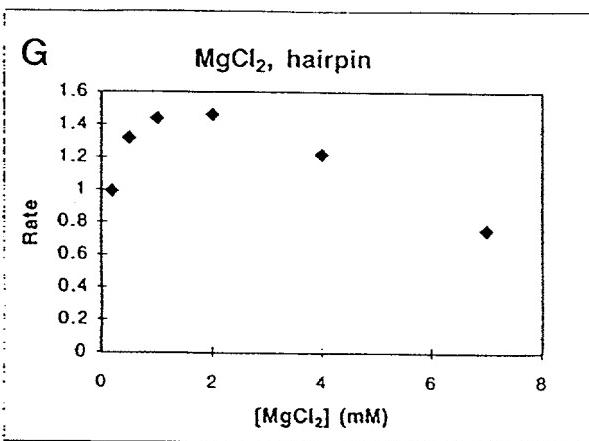
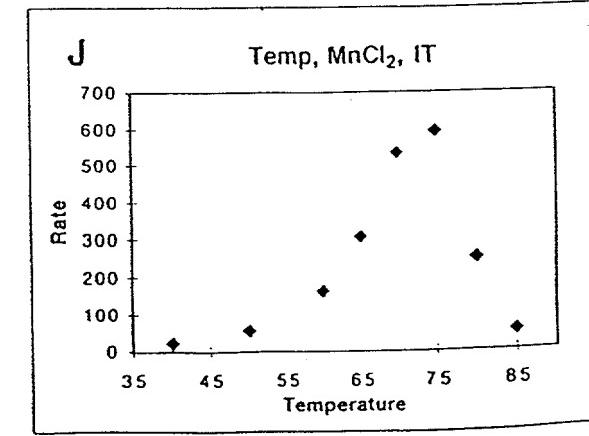
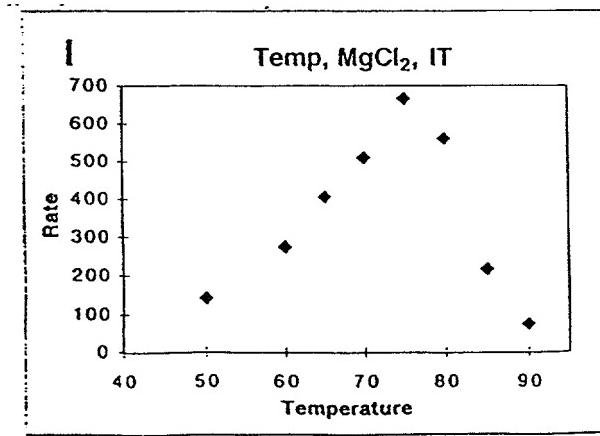
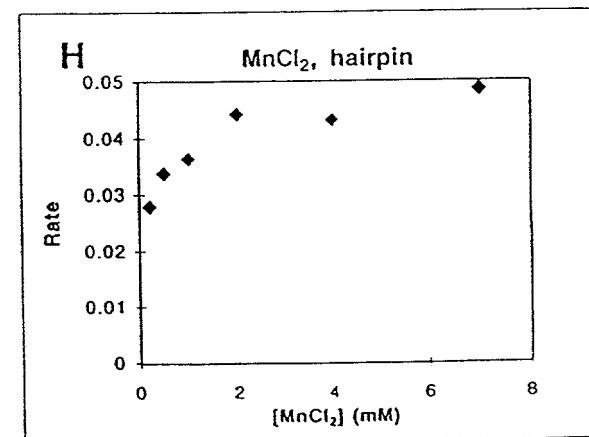
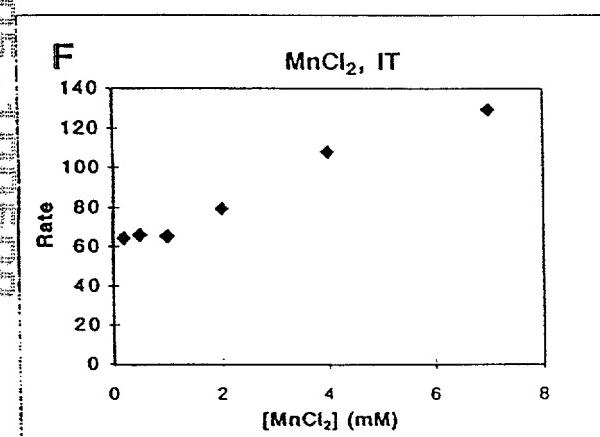
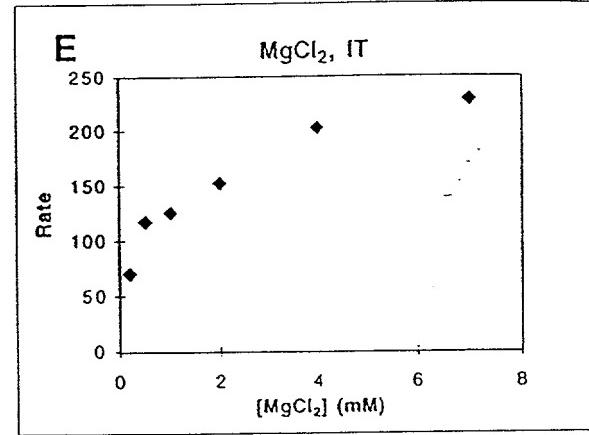
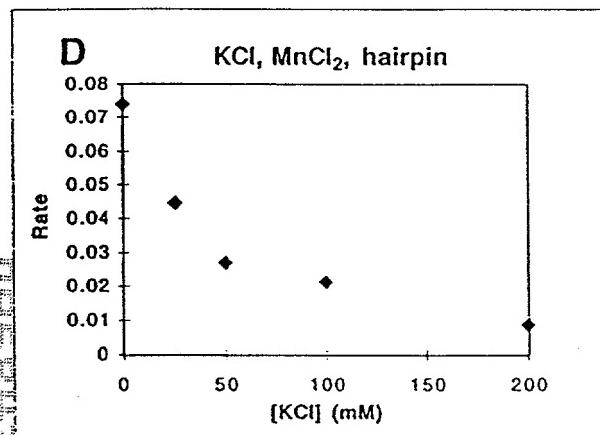
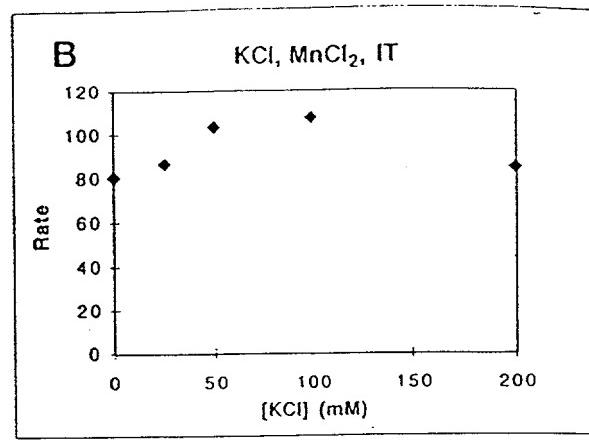
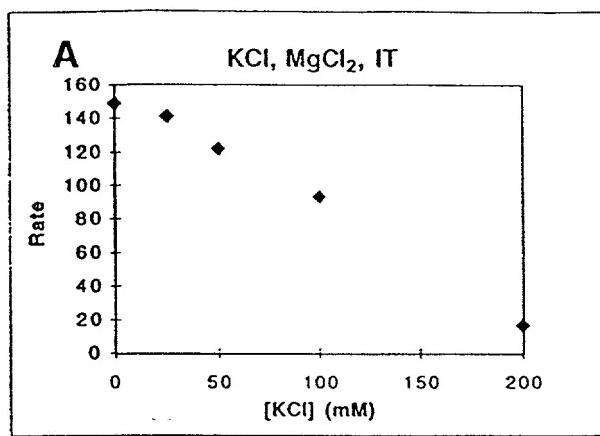


FIGURE 105



124/127

FIGURE 106

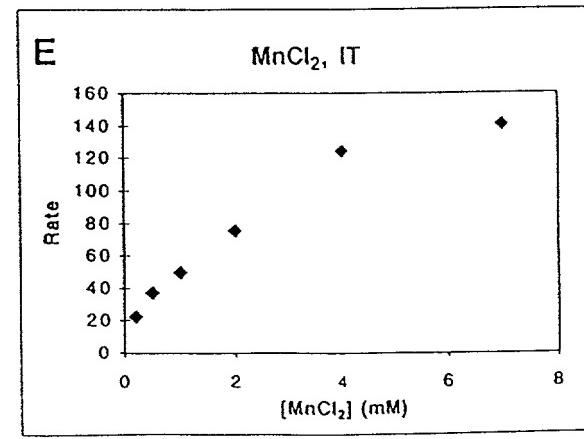
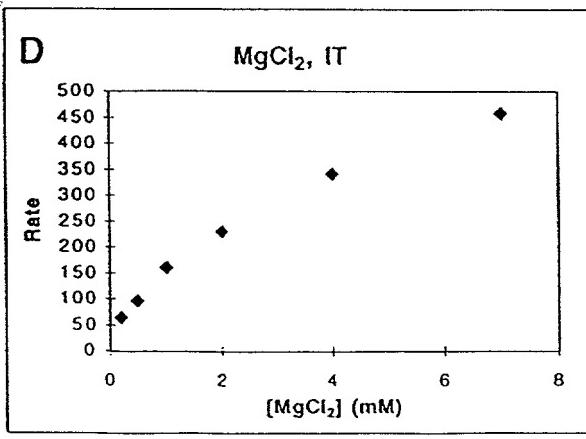
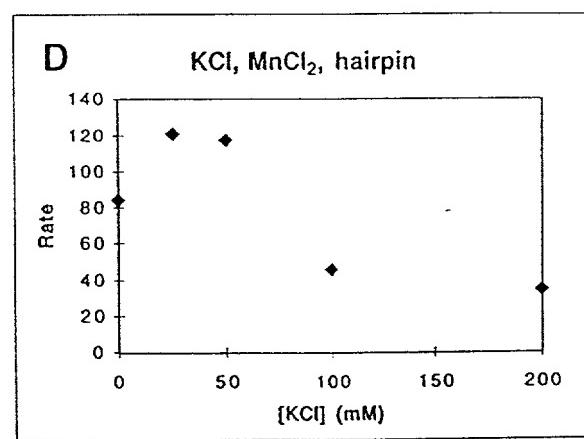
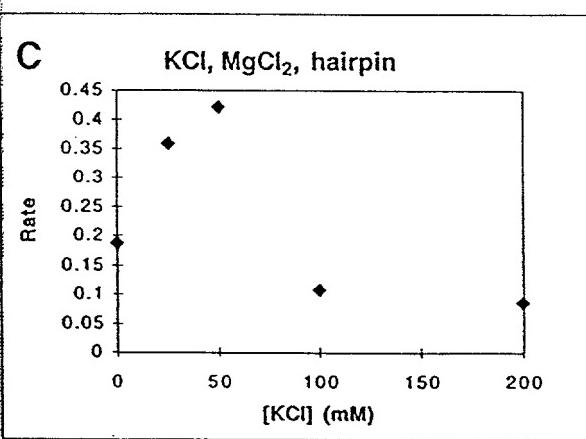
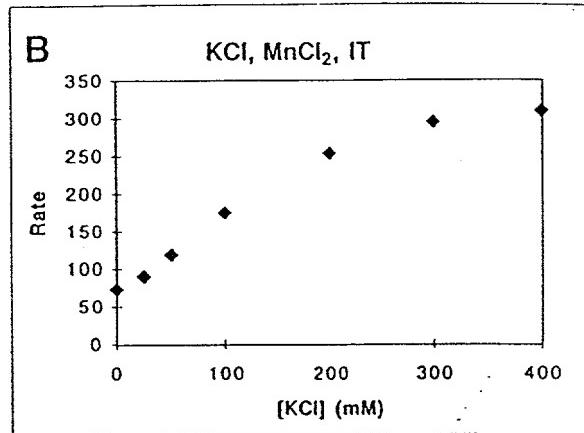
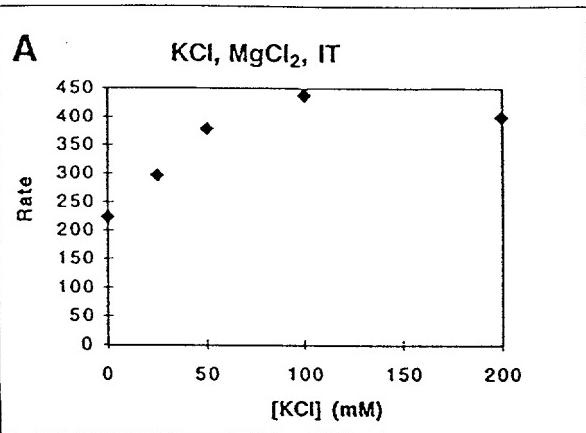
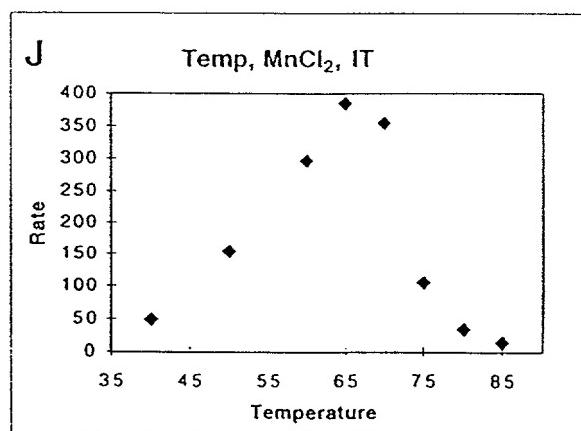
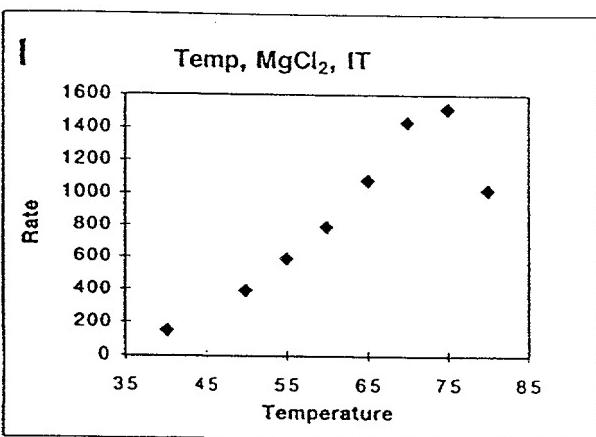
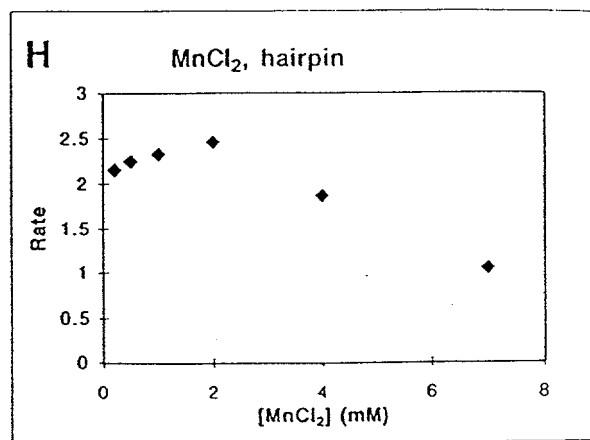
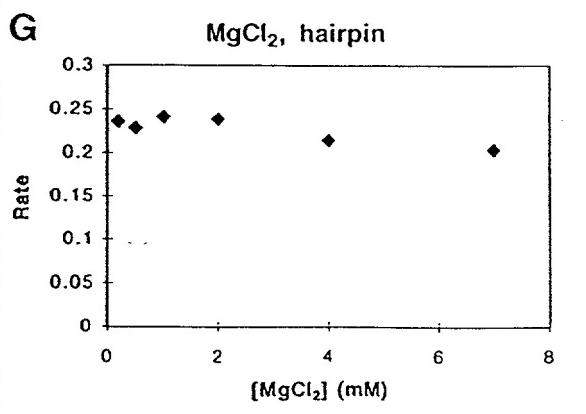


FIGURE 106 (cont.)

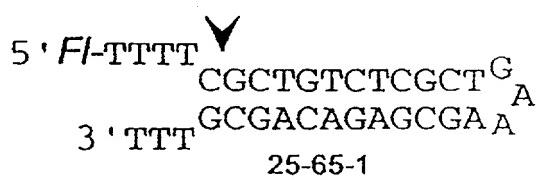


126/127

FIGURE 107

Hairpin Substrate

A)



B) Invader (IT) substrate

